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(54) Title: SPECIFIC AND UNIVERSAL PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN MICROBIOLOGY LABORATORIES			
(57) Abstract			
<p>The present invention relates to DNA-based methods for universal bacterial detection, for specific detection of the <i>pneumoniae</i>, <i>Pseudomonas aeruginosa</i>, <i>Proteus mirabilis</i>, <i>Streptococcus pneumoniae</i>, <i>Staphylococcus aureus</i>, <i>Staphylococcus epidermidis</i>, <i>Enterococcus faecalis</i>, <i>Staphylococcus saprophyticus</i>, <i>Streptococcus pyogenes</i>, <i>Haemophilus influenzae</i> and <i>Moraxella catarrhalis</i> as well as for specific detection of commonly encountered and clinically relevant bacterial antibiotic resistance genes directly from clinical specimens or, alternatively, from a bacterial colony. The above bacterial species can account for as much as 80 % of bacterial pathogens isolated in routine microbiology laboratories. The core of this invention consists primarily of the DNA sequences from all species-specific genomic DNA fragments selected by hybridization from genomic libraries or, alternatively, selected from data banks as well as any oligonucleotide sequences derived from these sequences which can be used as probes or amplification primers for PCR or any other nucleic acid amplification methods. This invention also includes DNA sequences from the selected clinically relevant antibiotic resistance genes.</p>			

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SPECIFIC AND UNIVERSAL PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN

5 MICROBIOLOGY LABORATORIES.

BACKGROUND OF THE INVENTION

Classical identification of bacteria

10 Bacteria are classically identified by their ability to utilize different substrates as a source of carbon and nitrogen through the use of biochemical tests such as the API20E™ system. Susceptibility testing of Gram negative bacilli has progressed to microdilution tests. Although the 15 API and the microdilution systems are cost-effective, at least two days are required to obtain preliminary results due to the necessity of two successive overnight incubations to isolate and identify the bacteria from the specimen. Some faster detection methods with sophisticated and expensive apparatus have been developed. For example, the fastest identification 20 system, the autoSCAN-Walk-Away™ system identifies both Gram negative and Gram positive from isolated bacterial colonies in 2 hours and susceptibility patterns to antibiotics in only 7 hours. However, this system has an unacceptable margin of 25 error, especially with bacterial species other than Enterobacteriaceae (York et al., 1992. J. Clin. Microbiol. 30:2903-2910). Nevertheless, even this fastest method requires primary isolation of the bacteria as a pure culture, a process which takes at least 18 hours if there is a pure culture or 2 30 to 3 days if there is a mixed culture.

Urine specimens

A large proportion (40-50%) of specimens received in routine diagnostic microbiology laboratories for bacterial 35 identification are urine specimens (Pezzlo, 1988, Clin. Microbiol. Rev. 1:268-280). Urinary tract infections (UTI) are extremely common and affect up to 20% of women and account for

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extensive morbidity and increased mortality among hospitalized patients (Johnson and Stamm, 1989; Ann. Intern. Med. 111:906-917). UTI are usually of bacterial etiology and require antimicrobial therapy. The Gram negative bacillus *Escherichia coli* is by far the most prevalent urinary pathogen and accounts for 50 to 60 % of UTI (Pezzlo, 1988, op. cit.). The prevalence for bacterial pathogens isolated from urine specimens observed recently at the "Centre Hospitalier de l'Université Laval (CHUL)" is given in Tables 1 and 2.

10

Conventional pathogen identification in urine specimens. The search for pathogens in urine specimens is so preponderant in the routine microbiology laboratory that a myriad of tests have been developed. The gold standard is still the classical 15 semi-quantitative plate culture method in which a calibrated loop of urine is streaked on plates and incubated for 18-24 hours. Colonies are then counted to determine the total number of colony forming units (CFU) per liter of urine. A bacterial count of $\geq 10^7$ UTI is normally associated with a bacterial count of $\geq 10^7$ 20 CFU/L in urine. However, infections with less than 10^7 CFU/L in urine are possible, particularly in patients with a high incidence of diseases or those catheterized (Stark and Maki, 1984, N. Engl. J. Med. 311:560-564). Importantly, close to 80% 25 of urine specimens tested are considered negative ($< 10^7$ CFU/L; Table 3).

Accurate and rapid urine screening methods for bacterial pathogens would allow a faster identification of negative results and a more efficient clinical investigation of the patient. Several rapid identification methods (Uriscreen™, 30 UTIscreen™, Flash Track™ DNA probes and others) were recently compared to slower standard biochemical methods which are based on culture of the bacterial pathogens. Although much faster, these rapid tests showed low sensitivities and specificities as well as a high number of false negative and 35 false positive results (Koenig et al., 1992. J. Clin. Microbiol. 30:342-345; Pezzlo et al., 1992. J. Clin. Microbiol. 30:640-684).

Urine specimens found positive by culture are further characterized using standard biochemical tests to identify the bacterial pathogen and are also tested for susceptibility to antibiotics.

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Any clinical specimens

As with urine specimen which was used here as an example, our probes and amplification primers are also applicable to any other clinical specimens. The DNA-based tests proposed in this invention are superior to standard methods currently used for routine diagnosis in terms of rapidity and accuracy. While a high percentage of urine specimens are negative, in many other clinical specimens more than 95% of cultures are negative (Table 4). These data further support the use of universal probes to screen out the negative clinical specimens. Clinical specimens from organisms other than humans (e.g. other primates, mammals, farm animals or live stocks) may also be used.

20 Towards the development of rapid DNA-based diagnostic tests

A rapid diagnostic test should have a significant impact on the management of infections. For the identification of pathogens and antibiotic resistance genes in clinical samples, DNA probe and DNA amplification technologies offer several advantages over conventional methods. There is no need for subculturing, hence the organism can be detected directly in clinical samples thereby reducing the costs and time associated with isolation of pathogens. DNA-based technologies have proven to be extremely useful for specific applications in the clinical microbiology laboratory. For example, kits for the detection of fastidious organisms based on the use of hybridization probes or DNA amplification for the direct detection of pathogens in clinical specimens are commercially available (Persing et al. 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

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The present invention is an advantageous alternative to the conventional culture identification methods used in hospital clinical microbiology laboratories and in private clinics for routine diagnosis. Besides being much faster, DNA-based diagnostic tests are more accurate than standard biochemical tests presently used for diagnosis because the bacterial genotype (e.g. DNA level) is more stable than the bacterial phenotype (e.g. biochemical properties). The originality of this invention is that genomic DNA fragments (size of at least 100 base pairs) specific for 12 species of commonly encountered bacterial pathogens were selected from genomic libraries or from data banks. Amplification primers or oligonucleotide probes (both less than 100 nucleotides in length) which are both derived from the sequence of species-specific DNA fragments identified by hybridization from genomic libraries or from selected data bank sequences are used as a basis to develop diagnostic tests. Oligonucleotide primers and probes for the detection of commonly encountered and clinically important bacterial resistance genes are also included. For example, Annexes I and II present a list of suitable oligonucleotide probes and PCR primers which were all derived from the species-specific DNA fragments selected from genomic libraries or from data bank sequences. It is clear to the individual skilled in the art that oligonucleotide sequences appropriate for the specific detection of the above bacterial species other than those listed in Annexes 1 and 2 may be derived from the species-specific fragments or from the selected data bank sequences. For example, the oligonucleotides may be shorter or longer than the ones we have chosen and may be selected anywhere else in the identified species-specific sequences or selected data bank sequences. Alternatively, the oligonucleotides may be designed for use in amplification methods other than PCR. Consequently, the core of this invention is the identification of species-specific genomic DNA fragments from bacterial genomic DNA libraries and the selection of genomic DNA fragments from data bank sequences which are used as a source of species-specific

and ubiquitous oligonucleotides. Although the selection of oligonucleotides suitable for diagnostic purposes from the sequence of the species-specific fragments or from the selected data bank sequences requires much effort it is quite possible for the individual skilled in the art to derive from our fragments or selected data bank sequences suitable oligonucleotides which are different from the ones we have selected and tested as examples (Annexes I and II).

Others have developed DNA-based tests for the detection and identification of some of the bacterial pathogens for which we have identified species-specific sequences (PCT patent application Serial No. WO 93/03186). However, their strategy was based on the amplification of the highly conserved 16S rRNA gene followed by hybridization with internal species-specific oligonucleotides. The strategy from this invention is much simpler and more rapid because it allows the direct amplification of species-specific targets using oligonucleotides derived from the species-specific bacterial genomic DNA fragments.

Since a high percentage of clinical specimens are negative, oligonucleotide primers and probes were selected from the highly conserved 16S or 23S rRNA genes to detect all bacterial pathogens possibly encountered in clinical specimens in order to determine whether a clinical specimen is infected or not. This strategy allows rapid screening out of the numerous negative clinical specimens submitted for bacteriological testing.

We are also developing other DNA-based tests, to be performed simultaneously with bacterial identification, to determine rapidly the putative bacterial susceptibility to antibiotics by targeting commonly encountered and clinically relevant bacterial resistance genes. Although the sequences from the selected antibiotic resistance genes are available and have been used to develop DNA-based tests for their detection (Ehrlich and Greenberg, 1994. PCR-based Diagnostics in Infectious Diseases, Blackwell Scientific Publications, Boston, Massachusetts; Persing et al, 1993. Diagnostic

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Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.), our approach is innovative as it represents major improvements over current "gold standard" diagnostic methods based on culture of the 5 bacteria because it allows the rapid identification of the presence of a specific bacterial pathogen and evaluation of its susceptibility to antibiotics directly from the clinical specimens within one hour.

We believe that the rapid and simple diagnostic tests not 10 based on cultivation of the bacteria that we are developing will gradually replace the slow conventional bacterial identification methods presently used in hospital clinical microbiology laboratories and in private clinics. In our opinion, these rapid DNA-based diagnostic tests for severe and 15 common bacterial pathogens and antibiotic resistance will (i) save lives by optimizing treatment, (ii) diminish antibiotic resistance by reducing the use of broad spectrum antibiotics and (iii) decrease overall health costs by preventing or shortening hospitalizations.

SUMMARY OF THE INVENTION

In accordance with the present invention, there is provided sequence from genomic DNA fragments (size of at least 5 100 base pairs and all described in the sequence listing) selected either by hybridization from genomic libraries or from data banks and which are specific for the detection of commonly encountered bacterial pathogens (i.e. *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Enterococcus faecalis*, *Staphylococcus saprophyticus*, *Streptococcus pyogenes*, *Haemophilus influenzae* and *Moraxella catarrhalis*) in clinical 10 15 specimens. These bacterial species are associated with approximately 90% of urinary tract infections and with a high percentage of other severe infections including septicemia, meningitis, pneumonia, intraabdominal infections, skin infections and many other severe respiratory tract infections. Overall, the above bacterial species may account for up to 80% 20 25 of bacterial pathogens isolated in routine microbiology laboratories.

Synthetic oligonucleotides for hybridization (probes) or DNA amplification (primers) were derived from the above species-specific DNA fragments (ranging in sizes from 0.25 to 5.0 kilobase pairs (kbp)) or from selected data bank sequences (GenBank and EMBL). Bacterial species for which some of the oligonucleotide probes and amplification primers were derived from selected data bank sequences are *Escherichia coli*, *Enterococcus faecalis*, *Streptococcus pyogenes* and *Pseudomonas aeruginosa*. The person skilled in the art understands that the 30 35 important innovation in this invention is the identification of the species-specific DNA fragments selected either from bacterial genomic libraries by hybridization or from data bank sequences. The selection of oligonucleotides from these fragments suitable for diagnostic purposes is also innovative. Specific and ubiquitous oligonucleotides different from the

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ones tested in the practice are considered as embodiments of the present invention.

The development of hybridization (with either fragment or oligonucleotide probes) or of DNA amplification protocols for 5 the detection of pathogens from clinical specimens renders possible a very rapid bacterial identification. This will greatly reduce the time currently required for the identification of pathogens in the clinical laboratory since these technologies can be applied for bacterial detection and 10 identification directly from clinical specimens with minimum pretreatment of any biological specimens to release bacterial DNA. In addition to being 100% specific, probes and amplification primers allow identification of the bacterial species directly from clinical specimens or, alternatively, 15 from an isolated colony. DNA amplification assays have the added advantages of being faster and more sensitive than hybridization assays, since they allow rapid and exponential in vitro replication of the target segment of DNA from the bacterial genome. Universal probes and amplification primers 20 selected from the 16S or 23S rRNA genes highly conserved among bacteria, which permit the detection of any bacterial pathogens, will serve as a procedure to screen out the numerous negative clinical specimens received in diagnostic laboratories. The use of oligonucleotide probes or primers 25 complementary to characterized bacterial genes encoding resistance to antibiotics to identify commonly encountered and clinically important resistance genes is also under the scope of this invention.

30

DETAILED DESCRIPTION OF THE INVENTION

Development of species-specific DNA probes

DNA fragment probes were developed for the following 35 bacterial species: *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Staphylococcus epidermidis*,

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5 *Staphylococcus saprophyticus*, *Haemophilus influenzae* and *Moraxella catarrhalis*. (For *Enterococcus faecalis* and *Streptococcus pyogenes*, oligonucleotide sequences were exclusively derived from selected data bank sequences). These species-specific fragments were selected from bacterial genomic libraries by hybridization to DNA from a variety of 10 Gram positive and Gram negative bacterial species (Table 5).

10 The chromosomal DNA from each bacterial species for which probes were sought was isolated using standard methods. DNA was digested with a frequently cutting restriction enzyme such as *Sau3AI* and then ligated into the bacterial plasmid vector pGEM3zf (Promega) linearized by appropriate restriction endonuclease digestion. Recombinant plasmids were then used to transform competent *E. coli* strain *DH5α* thereby yielding a 15 genomic library. The plasmid content of the transformed bacterial cells was analyzed using standard methods. DNA fragments of target bacteria ranging in size from 0.25 to 5.0 kilobase pairs (kbp) were cut out from the vector by digestion of the recombinant plasmid with various restriction 20 endonucleases. The insert was separated from the vector by agarose gel electrophoresis and purified in low melting point agarose gels. Each of the purified fragments of bacterial genomic DNA was then used as a probe for specificity tests.

25 For each given species, the gel-purified restriction fragments of unknown coding potential were labeled with the radioactive nucleotide α -³²P(dATP) which was incorporated into the DNA fragment by the random priming labeling reaction. Non-radioactive modified nucleotides could also be incorporated into the DNA by this method to serve as a label.

30 Each DNA fragment probe (i.e. a segment of bacterial genomic DNA of at least 100 bp in length cut out from clones randomly selected from the genomic library) was then tested for its specificity by hybridization to DNAs from a variety of bacterial species (Table 5). The double-stranded labeled DNA 35 probe was heat-denatured to yield labeled single-stranded DNA which could then hybridize to any single-stranded target DNA fixed onto a solid support or in solution. The target DNAs

consisted of total cellular DNA from an array of bacterial species found in clinical samples (Table 5). Each target DNA was released from the bacterial cells and denatured by conventional methods and then irreversibly fixed onto a solid support (e.g. nylon or nitrocellulose membranes) or free in solution. The fixed single-stranded target DNAs were then hybridized with the single-stranded probe. Pre-hybridization, hybridization and post-hybridization conditions were as follows: (i) Pre-hybridization; in 1 M NaCl + 10% dextran sulfate + 1% SDS (sodium dodecyl sulfate) + 100 µg/ml salmon sperm DNA at 65°C for 15 min. (ii) Hybridization; in fresh pre-hybridization solution containing the labeled probe at 65°C overnight. (iii) Post-hybridization; washes twice in 3X SSC containing 1% SDS (1X SSC is 0.15M NaCl, 0.015M NaCitrate) and twice in 0.1 X SSC containing 0.1% SDS; all washes were at 65°C for 15 min. Autoradiography of washed filters allowed the detection of selectively hybridized probes. Hybridization of the probe to a specific target DNA indicated a high degree of similarity between the nucleotide sequence of these two DNAs.

Species-specific DNA fragments selected from various bacterial genomic libraries ranging in size from 0.25 to 5.0 kbp were isolated for 10 common bacterial pathogens (Table 6) based on hybridization to chromosomal DNAs from a variety of bacteria performed as described above. All of the bacterial species tested (66 species listed in Table 5) were likely to be pathogens associated with common infections or potential contaminants which can be isolated from clinical specimens. A DNA fragment probe was considered specific only when it hybridized solely to the pathogen from which it was isolated.

DNA fragment probes found to be specific were subsequently tested for their ubiquity (i.e. ubiquitous probes recognized most isolates of the target species) by hybridization to bacterial DNAs from approximately 10 to 80 clinical isolates of the species of interest (Table 6). The DNAs were denatured, fixed onto nylon membranes and hybridized as described above.

Sequencing of the species-specific fragment probes

The nucleotide sequence of the totality or of a portion of the species-specific DNA fragments isolated (Table 6) was determined using the dideoxynucleotide termination sequencing method which was performed using Sequenase (USB Biochemicals) or T7 DNA polymerase (Pharmacia). These nucleotide sequences are shown in the sequence listing. Alternatively, sequences selected from data banks (GenBank and EMBL) were used as sources of oligonucleotides for diagnostic purposes for 5 *Escherichia coli*, *Enterococcus faecalis*, *Streptococcus pyogenes* and *Pseudomonas aeruginosa*. For this strategy, an array of suitable oligonucleotide primers or probes derived 10 from a variety of genomic DNA fragments (size of more than 100 bp) selected from data banks was tested for their specificity 15 and ubiquity in PCR and hybridization assays as described later. It is important to note that the data bank sequences were selected based on their potential of being species-specific according to available sequence information. Only 20 data bank sequences from which species-specific oligonucleotides could be derived are included in this invention.

Oligonucleotide probes and amplification primers derived from species-specific fragments selected from the genomic libraries or from data bank sequences were synthesized using 25 an automated DNA synthesizer (Millipore). Prior to synthesis, all oligonucleotides (probes for hybridization and primers for DNA amplification) were evaluated for their suitability for hybridization or DNA amplification by polymerase chain reaction (PCR) by computer analysis using standard programs 30 (e.g. Genetics Computer Group (GCG) and OligoTM 4.0 (National Biosciences)). The potential suitability of the PCR primer pairs was also evaluated prior to the synthesis by verifying the absence of unwanted features such as long stretches of one nucleotide, a high proportion of G or C residues at the 3' end 35 and a 3'-terminal T residue (Persing et al, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

Hybridization with oligonucleotide probes

In hybridization experiments, oligonucleotides (size less than 100 nucleotides) have some advantages over DNA fragment probes for the detection of bacteria such as ease of preparation in large quantities, consistency in results from batch to batch and chemical stability. Briefly, for the hybridizations, oligonucleotides were 5' end-labeled with the radionucleotide $\gamma^{32}\text{P}$ (ATP) using T4 polynucleotide kinase (Pharmacia). The unincorporated radionucleotide was removed by passing the labeled single-stranded oligonucleotide through a Sephadex G50 column. Alternatively, oligonucleotides were labeled with biotin, either enzymatically at their 3' ends or incorporated directly during synthesis at their 5' ends, or with digoxigenin. It will be appreciated by the person skilled in the art that labeling means other than the three above labels may be used.

The target DNA was denatured, fixed onto a solid support and hybridized as previously described for the DNA fragment probes. Conditions for pre-hybridization and hybridization were as described earlier. Post-hybridization washing conditions were as follows: twice in 3X SSC containing 1% SDS, twice in 2X SSC containing 1% SDS and twice in 1X SSC containing 1% SDS (all of these washes were at 65°C for 15 min), and a final wash in 0.1X SSC containing 1% SDS at 25°C for 15 min. For probes labeled with radioactive labels the detection of hybrids was by autoradiography as described earlier. For non-radioactive labels detection may be colorimetric or by chemiluminescence.

The oligonucleotide probes may be derived from either strand of the duplex DNA. The probes may consist of the bases A, G, C, or T or analogs. The probes may be of any suitable length and may be selected anywhere within the species-specific genomic DNA fragments selected from the genomic libraries or from data bank sequences.

DNA amplification

For DNA amplification by the widely used PCR (polymerase chain reaction) method, primer pairs were derived either from the sequenced species-specific DNA fragments or from data bank 5 sequences or, alternatively, were shortened versions of oligonucleotide probes. Prior to synthesis, the potential primer pairs were analyzed by using the program OligoTM 4.0 (National Biosciences) to verify that they are likely candidates for PCR amplifications.

10 During DNA amplification by PCR, two oligonucleotide primers binding respectively to each strand of the denatured double-stranded target DNA from the bacterial genome are used to amplify exponentially *in vitro* the target DNA by successive thermal cycles allowing denaturation of the DNA, annealing of 15 the primers and synthesis of new targets at each cycle (Persing et al, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). Briefly, the PCR protocols were as follows. Clinical specimens or bacterial colonies were 20 added directly to the 50 µL PCR reaction mixtures containing 50 mM KCl, 10 mM Tris-HCl pH 8.3, 2.5 mM MgCl₂, 0.4 µM of each of the two primers, 200 µM of each of the four dNTPs and 1.25 Units of Tag DNA polymerase (Perkin Elmer). PCR reactions were then subjected to thermal cycling (3 min at 95°C followed by 25 30 cycles of 1 second at 95°C and 1 second at 55°C) using a Perkin Elmer 480TM thermal cycler and subsequently analyzed by standard ethidium bromide-stained agarose gel electrophoresis. It is clear that other methods for the detection of specific amplification products, which may be faster and more practical 30 for routine diagnosis, may be used. Such methods may be based on the detection of fluorescence after amplification (e.g. TaqManTM system from Perkin Elmer or AmplisensorTM from Biotronics) or liquid hybridization with an oligonucleotide probe binding to internal sequences of the specific 35 amplification product. These novel probes can be generated from our species-specific fragment probes. Methods based on the detection of fluorescence are particularly promising for

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utilization in routine diagnosis as they are, very rapid and quantitative and can be automated.

To assure PCR efficiency, glycerol or dimethyl sulfoxide (DMSO) or other related solvents, can be used to increase the sensitivity of the PCR and to overcome problems associated with the amplification of target with a high GC content or with strong secondary structures. The concentration ranges for glycerol and DMSO are 5-15% (v/v) and 3-10% (v/v), respectively. For the PCR reaction mixture, the concentration ranges for the amplification primers and the MgCl₂ are 0.1-1.0 μM and 1.5-3.5 mM, respectively. Modifications of the standard PCR protocol using external and nested primers (i.e. nested PCR) or using more than one primer pair (i.e. multiplex PCR) may also be used (Persing et al, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). For more details about the PCR protocols and amplicon detection methods see examples 7 and 8.

The person skilled in the art of DNA amplification knows the existence of other rapid amplification procedures such as ligase chain reaction (LCR), transcription-based amplification systems (TAS), self-sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA) and branched DNA (bDNA) (Persing et al, 1993. Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). The scope of this invention is not limited to the use of amplification by PCR, but rather includes the use of any rapid nucleic acid amplification methods or any other procedures which may be used to increase rapidity and sensitivity of the tests. Any oligonucleotides suitable for the amplification of nucleic acid by approaches other than PCR and derived from the species-specific fragments and from selected antibiotic resistance gene sequences included in this document are also under the scope of this invention.

Specificity and ubiquity tests for oligonucleotide probes and primers

The specificity of oligonucleotide probes, derived either from the sequenced species-specific fragments or from data bank sequences, was tested by hybridization to DNAs from the array of bacterial species listed in Table 5 as previously described. Oligonucleotides found to be specific were subsequently tested for their ubiquity by hybridization to bacterial DNAs from approximately 80 isolates of the target species as described for fragment probes. Probes were considered ubiquitous when they hybridized specifically with the DNA from at least 80% of the isolates. Results for specificity and ubiquity tests with the oligonucleotide probes are summarized in Table 6. The specificity and ubiquity of the amplification primer pairs were tested directly from cultures (see example 7) of the same bacterial strains. For specificity and ubiquity tests, PCR assays were performed directly from bacterial colonies of approximately 80 isolates of the target species. Results are summarized in Table 7. All specific and ubiquitous oligonucleotide probes and amplification primers for each of the 12 bacterial species investigated are listed in Annexes I and II, respectively. Divergence in the sequenced DNA fragments can occur and, insofar as the divergence of these sequences or a part thereof does not affect the specificity of the probes or amplification primers, variant bacterial DNA is under the scope of this invention.

Universal bacterial detection

In the routine microbiology laboratory a high percentage of clinical specimens sent for bacterial identification is negative (Table 4). For example, over a 2 year period, around 5 80% of urine specimens received by the laboratory at the "Centre Hospitalier de l'Université Laval (CHUL)" were negative (i.e. $<10^7$ CFU/L) (Table 3). Testing clinical samples with universal probes or universal amplification primers to detect the presence of bacteria prior to specific 10 identification and screen out the numerous negative specimens is thus useful as it saves costs and may rapidly orient the clinical management of the patients. Several oligonucleotides and amplification primers were therefore synthesized from highly conserved portions of bacterial 16S or 23S ribosomal 15 RNA gene sequences available in data banks (Annexes III and IV). In hybridization tests, a pool of seven oligonucleotides (Annex I; Table 6) hybridized strongly to DNA from all bacterial species listed in Table 5. This pool of universal probes labeled with radionucleotides or with any other 20 modified nucleotides is consequently very useful for detection of bacteria in urine samples with a sensitivity range of $\geq 10^7$ CFU/L. These probes can also be applied for bacterial detection in other clinical samples.

Amplification primers also derived from the sequence of 25 highly conserved ribosomal RNA genes were used as an alternative strategy for universal bacterial detection directly from clinical specimens (Annex IV; Table 7). The DNA amplification strategy was developed to increase the sensitivity and the rapidity of the test. This amplification 30 test was ubiquitous since it specifically amplified DNA from 23 different bacterial species encountered in clinical specimens.

Well-conserved bacterial genes other than ribosomal RNA 35 genes could also be good candidates for universal bacterial detection directly from clinical specimens. Such genes may be associated with processes essential for bacterial survival (e.g. protein synthesis, DNA synthesis, cell division or DNA

repair) and could therefore be highly conserved during evolution. We are working on these candidate genes to develop new rapid tests for the universal detection of bacteria directly from clinical specimens.

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Antibiotic resistance genes

Antimicrobial resistance complicates treatment and often leads to therapeutic failures. Furthermore, overuse of antibiotics inevitably leads to the emergence of bacterial 10 resistance. Our goal is to provide the clinicians, within one hour, the needed information to prescribe optimal treatments. Besides the rapid identification of negative clinical specimens with DNA-based tests for universal bacterial detection and the identification of the presence of a specific 15 pathogen in the positive specimens with DNA-based tests for specific bacterial detection, the clinicians also need timely information about the ability of the bacterial pathogen to resist antibiotic treatments. We feel that the most efficient strategy to evaluate rapidly bacterial resistance to 20 antimicrobials is to detect directly from the clinical specimens the most common and important antibiotic resistance genes (i.e. DNA-based tests for the detection of antibiotic resistance genes). Since the sequence from the most important and common bacterial antibiotic resistance genes are available 25 from data banks, our strategy is to use the sequence from a portion or from the entire gene to design specific oligonucleotides which will be used as a basis for the development of rapid DNA-based tests. The sequence from the bacterial antibiotic resistance genes selected on the basis of 30 their clinical relevance (i.e. high incidence and importance) is given in the sequence listing. Table 8 summarizes some characteristics of the selected antibiotic resistance genes.

EXAMPLES

The following examples are intended to be illustrative of the various methods and compounds of the invention.

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EXAMPLE 1:

Isolation and cloning of fragments. Genomic DNAs from *Escherichia coli* strain ATCC 25922, *Klebsiella pneumoniae* strain CK2, *Pseudomonas aeruginosa* strain ATCC 27853, *Proteus mirabilis* strain ATCC 35657, *Streptococcus pneumoniae* strain ATCC 27336, *Staphylococcus aureus* strain ATCC 25923, *Staphylococcus epidermidis* strain ATCC 12228, *Staphylococcus saprophyticus* strain ATCC 15305, *Haemophilus influenzae* reference strain Rd and *Moraxella catarrhalis* strain ATCC 53879 were prepared using standard procedures. It is understood that the bacterial genomic DNA may have been isolated from strains other than the ones mentioned above. (For *Enterococcus faecalis* and *Streptococcus pyogenes* oligonucleotide sequences were derived exclusively from data banks). Each DNA was digested with a restriction enzyme which frequently cuts DNA such as Sau3AI. The resulting DNA fragments were ligated into a plasmid vector (pGEM3Zf) to create recombinant plasmids and transformed into competent *E. coli* cells (DH5 α). It is understood that the vectors and corresponding competent cells should not be limited to the ones herein above specifically exemplified. The objective of obtaining recombinant plasmids and transformed cells is to provide an easily reproducible source of DNA fragments useful as probes. Therefore, insofar as the inserted fragments are specific and selective for the target bacterial DNA, any recombinant plasmids and corresponding transformed host cells are under the scope of this invention. The plasmid content of the transformed bacterial cells was analyzed using standard methods. DNA fragments from target bacteria ranging in size from 0.25 to 5.0 kbp were cut out from the vector by digestion of the recombinant plasmid with various restriction endonucleases. The insert was separated from the vector by

agarose gel electrophoresis and purified in a low melting point agarose gel. Each of the purified fragments was then used for specificity tests.

5 Labeling of DNA fragment probes. The label used was $\alpha^{32}\text{P}(\text{dATP})$, a radioactive nucleotide which can be incorporated enzymatically into a double-stranded DNA molecule. The fragment of interest is first denatured by heating at 95°C for 5 min, then a mixture of random primers is allowed to anneal 10 to the strands of the fragments. These primers, once annealed, provide a starting point for synthesis of DNA. DNA polymerase, usually the Klenow fragment, is provided along with the four nucleotides, one of which is radioactive. When the reaction is terminated, the mixture of new DNA molecules is once again 15 denatured to provide radioactive single-stranded DNA molecules (i.e. the probe). As mentioned earlier, other modified nucleotides may be used to label the probes.

20 Specificity and ubiquity tests for the DNA fragment probes. Species-specific DNA fragments ranging in size from 0.25 to 5.0 kbp were isolated for 10 common bacterial pathogens (Table 6) based on hybridization to chromosomal DNAs from a variety of bacteria. Samples of whole cell DNA for each bacterial strain listed in Table 5 were transferred onto a 25 nylon membrane using a dot blot apparatus, washed and denatured before being irreversibly fixed. Hybridization conditions were as described earlier. A DNA fragment probe was considered specific only when it hybridized solely to the pathogen from which it was isolated. Labeled DNA fragments 30 hybridizing specifically only to target bacterial species (i.e. specific) were then tested for their ubiquity by hybridization to DNAs from approximately 10 to 80 isolates of the species of interest as described earlier. The conditions for pre-hybridization, hybridization and post-hybridization 35 washes were as described earlier. After autoradiography (or other detection means appropriate for the non-radioactive label used), the specificity of each individual probe can be

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determined. Each probe found to be specific (i.e. hybridizing only to the DNA from the bacterial species from which it was isolated) and ubiquitous (i.e. hybridizing to most isolates of the target species) was kept for further experimentations.

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EXAMPLE 2:

Same as example 1 except that testing of the strains is by colony hybridization. The bacterial strains were inoculated onto a nylon membrane placed on nutrient agar. The membranes 10 were incubated at 37°C for two hours and then bacterial lysis and DNA denaturation were carried out according to standard procedures. DNA hybridization was performed as described earlier.

15 **EXAMPLE 3:**

Same as example 1 except that bacteria were detected directly from clinical samples. Any biological samples were loaded directly onto a dot blot apparatus and cells were lysed in situ for bacterial detection. Blood samples should be 20 heparinized in order to avoid coagulation interfering with their convenient loading on a dot blot apparatus.

EXAMPLE 4:

Nucleotide sequencing of DNA fragments. The nucleotide 25 sequence of the totality or a portion of each fragment found to be specific and ubiquitous (Example 1) was determined using the dideoxynucleotide termination sequencing method (Sanger et al., 1977, Proc. Natl. Acad. Sci. USA. 74:5463-5467). These DNA sequences are shown in the sequence listing. 30 Oligonucleotide probes and amplification primers were selected from these nucleotide sequences, or alternatively, from selected data banks sequences and were then synthesized on an automated Biosearch synthesizer (Millipore™) using phosphoramidite chemistry.

35

Labeling of oligonucleotides. Each oligonucleotide was 5' end-labeled with $\gamma^{32}\text{P}$ -ATP by the T4 polynucleotide kinase

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(Pharmacia) as described earlier. The label could also be non-radioactive.

Specificity test for oligonucleotide probes. All labeled 5 oligonucleotide probes were tested for their specificity by hybridization to DNAs from a variety of Gram positive and Gram negative bacterial species as described earlier. Species-specific probes were those hybridizing only to DNA from the bacterial species from which it was isolated. Oligonucleotide 10 probes found to be specific were submitted to ubiquity tests as follows.

Ubiquity test for oligonucleotide probes. Specific 15 oligonucleotide probes were then used in ubiquity tests with approximately 80 strains of the target species. Chromosomal DNAs from the isolates were transferred onto nylon membranes and hybridized with labeled oligonucleotide probes as described for specificity tests. The batteries of approximately 80 isolates constructed for each target species 20 contain reference ATCC strains as well as a variety of clinical isolates obtained from various sources. Ubiquitous probes were those hybridizing to at least 80% of DNAs from the battery of clinical isolates of the target species. Examples of specific and ubiquitous oligonucleotide probes are listed 25 in Annex 1.

EXAMPLE 5:

Same as example 4 except that a pool of specific 30 oligonucleotide probes is used for bacterial identification (i) to increase sensitivity and assure 100% ubiquity or (ii) to identify simultaneously more than one bacterial species. Bacterial identification could be done from isolated colonies or directly from clinical specimens.

35 EXAMPLE 6:

PCR amplification. The technique of PCR was used to increase sensitivity and rapidity of the tests. The PCR

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primers used were often shorter derivatives of the extensive sets of oligonucleotides previously developed for hybridization assays (Table 6). The sets of primers were tested in PCR assays performed directly from a bacterial 5 colony or from a bacterial suspension (see Example 7) to determine their specificity and ubiquity (Table 7). Examples of specific and ubiquitous PCR primer pairs are listed in annex II.

10 Specificity and ubiquity tests for amplification primers.

The specificity of all selected PCR primer pairs was tested against the battery of Gram negative and Gram positive bacteria used to test the oligonucleotide probes (Table 5). Primer pairs found specific for each species were then tested 15 for their ubiquity to ensure that each set of primers could amplify at least 80% of DNAs from a battery of approximately 80 isolates of the target species. The batteries of isolates constructed for each species contain reference ATCC strains and various clinical isolates representative of the clinical 20 diversity for each species.

Standard precautions to avoid false positive PCR results should be taken. Methods to inactivate PCR amplification products such as the inactivation by uracil-N-glycosylase may be used to control PCR carryover.

25

EXAMPLE 7:

Amplification directly from a bacterial colony or suspension. PCR assays were performed either directly from a bacterial colony or from a bacterial suspension, the latter 30 being adjusted to a standard McFarland 0.5 (corresponds to 1.5 x 10⁸ bacteria/mL). In the case of direct amplification from a colony, a portion of the colony was transferred directly to a 50 µL PCR reaction mixture (containing 50 mM KCl, 10 mM Tris pH 8.3, 2.5 mM MgCl₂, 0.4 µM of each of the two primers, 200 35 µM of each of the four dNTPs and 1.25 Unit of Taq DNA polymerase (Perkin Elmer)) using a plastic rod. For the bacterial suspension, 4 µL of the cell suspension was added to

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46 μ L of the same PCR reaction mixture. For both strategies, the reaction mixture was overlaid with 50 μ L of mineral oil and PCR amplifications were carried out using an initial denaturation step of 3 min. at 95°C followed by 30 cycles 5 consisting of a 1 second denaturation step at 95°C and of a 1 second annealing step at 55°C in a Perkin Elmer 480™ thermal cycler. PCR amplification products were then analyzed by standard agarose gel (2%) electrophoresis. Amplification products were visualized in agarose gels containing 2.5 μ g/mL 10 of ethidium bromide under UV at 254 nm. The entire PCR assay can be completed in approximately one hour.

10 Alternatively, amplification from bacterial cultures was performed as described above but using a "hot start" protocol. In that case, an initial reaction mixture containing the 15 target DNA, primers and dNTPs was heated at 85°C prior to the addition of the other components of the PCR reaction mixture. The final concentration of all reagents was as described above. Subsequently, the PCR reactions were submitted to thermal cycling and analysis as described above.

20

EXAMPLE 8:

25 Amplification directly from clinical specimens. For amplification from urine specimens, 4 μ L of undiluted or diluted (1:10) urine was added directly to 46 μ L of the above PCR reaction mixture and amplified as described earlier.

30 To improve bacterial cell lysis and eliminate the PCR inhibitory effects of clinical specimens, samples were routinely diluted in lysis buffer containing detergent(s). Subsequently, the lysate was added directly to the PCR reaction mixture. Heat treatments of the lysates, prior to DNA amplification, using the thermocycler or a microwave oven could also be performed to increase the efficiency of cell lysis.

35 Our strategy is to develop rapid and simple protocols to eliminate PCR inhibitory effects of clinical specimens and lyse bacterial cells to perform DNA amplification directly from a variety of biological samples. PCR has the advantage of

being compatible with crude DNA preparations. For example, blood, cerebrospinal fluid and sera may be used directly in PCR assays after a brief heat treatment. We intend to use such rapid and simple strategies to develop fast protocols for DNA amplification from a variety of clinical specimens.

EXAMPLE 9:

Detection of antibiotic resistance genes. The presence of specific antibiotic resistance genes which are frequently encountered and clinically relevant is identified using the PCR amplification or hybridization protocols described in previous sections. Specific oligonucleotides used as a basis for the DNA-based tests are selected from the antibiotic resistance gene sequences. These tests can be performed either directly from clinical specimens or from a bacterial colony and should complement diagnostic tests for specific bacterial identification.

EXAMPLE 10:

Same as examples 7 and 8 except that assays were performed by multiplex PCR (i.e. using several pairs of primers in a single PCR reaction) to (i) reach an ubiquity of 100% for the specific target pathogen or (ii) to detect simultaneously several species of bacterial pathogens.

For example, the detection of *Escherichia coli* requires three pairs of PCR primers to assure a ubiquity of 100%. Therefore, a multiplex PCR assay (using the "hot-start" protocol (Example 7)) with those three primer pairs was developed. This strategy was also used for the other bacterial pathogens for which more than one primer pair was required to reach an ubiquity of 100%.

Multiplex PCR assays could also be used to (i) detect simultaneously several bacterial species or, alternatively, (ii) to simultaneously identify the bacterial pathogen and detect specific antibiotic resistance genes either directly from a clinical specimen or from a bacterial colony.

For these applications, amplicon detection methods should be adapted to differentiate the various amplicons produced. Standard agarose gel electrophoresis could be used because it discriminates the amplicons based on their sizes. Another 5 useful strategy for this purpose would be detection using a variety of fluorochromes emitting at different wavelengths which are each coupled with a specific oligonucleotide linked to a fluorescence quencher which is degraded during amplification to release the fluorochrome (e.g. TaqManTM, 10 Perkin Elmer).

EXAMPLE 11:

Detection of amplification products. The person skilled in the art will appreciate that alternatives other than standard 15 agarose gel electrophoresis (Example 7) may be used for the revelation of amplification products. Such methods may be based on the detection of fluorescence after amplification (e.g. AmplisensorTM, Biotronics; TaqManTM) or other labels such as biotin (SHARP SignalTM system, Digene Diagnostics). 20 These methods are quantitative and easily automated. One of the amplification primers or an internal oligonucleotide probe specific to the amplicon(s) derived from the species-specific fragment probes is coupled with the fluorochrome or with any other label. Methods based on the detection of fluorescence 25 are particularly suitable for diagnostic tests since they are rapid and flexible as fluorochromes emitting different wavelengths are available (Perkin Elmer).

EXAMPLE 12:

30 Species-specific, universal and antibiotic resistance gene amplification primers can be used in other rapid amplification procedures such as the ligase chain reaction (LCR), transcription-based amplification systems (TAS), self-sustained sequence replication (3SR), nucleic acid sequence-35 based amplification (NASBA), strand displacement amplification (SDA) and branched DNA (bDNA) or any other methods to increase the sensitivity of the test. Amplifications can be performed

from an isolated bacterial colony or directly from clinical specimens. The scope of this invention is therefore not limited to the use of PCR but rather includes the use of any procedures to specifically identify bacterial DNA and which 5 may be used to increase rapidity and sensitivity of the tests.

EXAMPLE 13:

A test kit would contain sets of probes specific for each bacterium as well as a set of universal probes. The kit is 10 provided in the form of test components, consisting of the set of universal probes labeled with non-radioactive labels as well as labeled specific probes for the detection of each bacterium of interest in specific clinical samples. The kit will also include test reagents necessary to perform the pre- 15 hybridization, hybridization, washing steps and hybrid detection. Finally, test components for the detection of known antibiotic resistance genes (or derivatives therefrom) will be included. Of course, the kit will include standard samples to be used as negative and positive controls for each 20 hybridization test.

Components to be included in the kits will be adapted to each specimen type and to detect pathogens commonly encountered in that type of specimen. Reagents for the universal detection of bacteria will also be included. Based 25 on the sites of infection, the following kits for the specific detection of pathogens may be developed:

-A kit for the universal detection of bacterial pathogens from most clinical specimens which contains sets of probes specific for highly conserved regions of the bacterial 30 genomes.

-A kit for the detection of bacterial pathogens retrieved from urine samples, which contains eight specific test components (sets of probes for the detection of *Escherichia coli*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Proteus mirabilis*, *Pseudomonas aeruginosa*, *Staphylococcus saprophyticus*, *Staphylococcus aureus* and *Staphylococcus epidermidis*).

-A kit for the detection of respiratory pathogens which contains seven specific test components (sets of probes for detecting *Streptococcus pneumoniae*, *Moraxella catarrhalis*, *Haemophilus influenzae*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Streptococcus pyogenes* and *Staphylococcus aureus*).

5 -A kit for the detection of pathogens retrieved from blood samples, which contains eleven specific test components (sets of probes for the detection of *Streptococcus pneumoniae*, *Moraxella catarrhalis*, *Haemophilus influenzae*, *Proteus mirabilis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Escherichia coli*, *Enterococcus faecalis*, *Staphylococcus aureus*, *Streptococcus pyogenes* and *Staphylococcus epidermidis*).

10 -A kit for the detection of pathogens causing meningitis, which contains four specific test components (sets of probes for the detection of *Haemophilus influenzae*, *Streptococcus pneumoniae*, *Escherichia coli* and *Pseudomonas aeruginosa*).

15 -A kit for the detection of clinically important antibiotic resistance genes which contains sets of probes for the specific detection of at least one of the 19 following genes associated with bacterial resistance : *blatem*, *blarob*, *blashv*, *aadB*, *aacC1*, *aacC2*, *aacC3*, *aacA4*, *mecA*, *vanA*, *vanH*, *vanX*, *satA*, *aacA-aphD*, *vat*, *vga*, *msrA*, *sul* and *int*.

20 -Other kits adapted for the detection of pathogens from skin, abdominal wound or any other clinically relevant kits will be developed.

EXAMPLE 14:

25 Same as example 13 except that the test kits contain all reagents and controls to perform DNA amplification assays. Diagnostic kits will be adapted for amplification by PCR (or other amplification methods) performed directly either from clinical specimens or from a bacterial colony. Components required for universal bacterial detection, bacterial identification and antibiotic resistance genes detection will be included.

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Amplification assays could be performed either in tubes or in microtitration plates having multiple wells. For assays in plates, the wells will be coated with the specific amplification primers and control DNAs and the detection of 5 amplification products will be automated. Reagents and amplification primers for universal bacterial detection will be included in kits for tests performed directly from clinical specimens. Components required for bacterial identification and antibiotic resistance gene detection will be included in 10 kits for testing directly from colonies as well as in kits for testing directly from clinical specimens.

The kits will be adapted for use with each type of specimen as described in example 13 for hybridization-based diagnostic kits.

15

EXAMPLE 15:

It is understood that the use of the probes and amplification primers described in this invention for bacterial detection and identification is not limited to 20 clinical microbiology applications. In fact, we feel that other sectors could also benefit from these new technologies. For example, these tests could be used by industries for quality control of food, water, pharmaceutical products or other products requiring microbiological control. These tests 25 could also be applied to detect and identify bacteria in biological samples from organisms other than humans (e.g. other primates, mammals, farm animals and live stocks). These diagnostic tools could also be very useful for research purposes including clinical trials and epidemiological 30 studies.

Table 1. Distribution of urinary isolates from positive urine samples ($\geq 10^7$ CFU/L) at the Centre Hospitalier de l'Université Laval (CHUL) for the 1992-1994 period.

		% of isolates			
	Organisms	Nov 92 n=267 ^a	Apr 93 n=265	Jul 93 n=238	Jan 94 n=281
10	<i>Escherichia coli</i>	53.2	51.7	53.8	54.1
	<i>Enterococcus faecalis</i>	13.8	12.4	11.7	11.4
15	<i>Klebsiella pneumoniae</i>	6.4	6.4	5.5	5.3
	<i>Staphylococcus epidermidis</i>	7.1	7.9	3.0	6.4
	<i>Proteus mirabilis</i>	2.6	3.4	3.8	2.5
	<i>Pseudomonas aeruginosa</i>	3.7	3.0	5.0	2.9
	<i>Staphylococcus saprophyticus</i>	3.0	1.9	5.4	1.4
20	Others ^b	10.2	13.3	11.8	16.0

^a n = total number of isolates for the indicated month.

^b See Table 2.

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Table 2. Distribution of uncommon^a urinary isolates from positive urine samples ($\geq 10^7$ CFU/L) at the Centre Hospitalier de l'Université Laval (CHUL) for the 1992-1994 period.

10	Organisms ^a	% of isolates			
		Nov 92	Apr 93	Jul 93	Jan 94
	<i>Staphylococcus aureus</i>	0.4	1.1	1.3	1.4
	<i>Staphylococcus spp.</i>	2.2	4.9	1.7	6.0
15	<i>Micrococcus spp.</i>	0.0	0.0	0.4	0.7
	<i>Enterococcus faecium</i>	0.4	0.4	1.3	1.4
	<i>Citrobacter spp.</i>	1.4	0.8	0.4	0.7
	<i>Enterobacter spp.</i>	1.5	1.1	1.3	1.4
	<i>Klebsiella oxytoca</i>	1.1	1.5	2.5	1.8
20	<i>Serratia spp.</i>	0.8	0.0	0.5	0.0
	<i>Proteus spp.</i>	0.4	0.4	0.0	1.1
	<i>Morganella</i> and <i>Providencia</i>	0.4	0.8	0.4	0.0
	<i>Hafnia alvei</i>	0.8	0.0	0.0	0.0
	<i>NFB^b</i>	0.0	0.4	1.3	1.1
25	<i>Candida spp.</i>	0.8	1.9	0.7	0.4

^a Uncommon urinary isolates are those identified as "Others" in Table 1.

^b NFB: non fermentative bacilli (i.e. *Stenotrophomonas* and *Acinetobacter*).

5 **Table 3. Distribution of positive^a (bacterial count $\geq 10^7$ CFU/L) and negative (bacterial count $< 10^7$ CFU/L) urine specimens tested at the Centre Hospitalier de l'Université Laval (CHUL) for the 1992-1994 period.**

10	Specimens	Number of isolates (%)			
		Nov 92	Apr 93	Jul 93	Jan 94
15	received:	1383(100)	1338(100)	1139(100)	1345(100)
	positive:	267(19.3)	265(19.8)	238(20.9)	281(20.9)
	negative:	1116(80.7)	1073(80.2)	901(79.1)	1064(79.1)

^a Based on standard diagnostic methods, the minimal number of bacterial pathogens in urine samples to indicate an urinary tract infection is normally 10^7 CFU/L.

Table 4. Distribution of positive and negative clinical specimens tested in the Microbiology Laboratory of the CHUL.

5

	Clinical specimens ^a	No. of samples tested	% of negative specimens	% of positive specimens
10				
	Urine	17,981	19.4	80.6
	Haemoculture/marrow	10,010	6.9	93.1
	Sputum	1,266	68.4	31.6
15	Superficial pus	1,136	72.3	27.7
	Cerebrospinal fluid	553	1.0	99.0
	Synovial fluid-articular	523	2.7	97.3
	Bronch./Trach./Amyg./Throat	502	56.6	43.4
	Deep pus	473	56.8	43.2
20	Ears	289	47.1	52.9
	Pleural and pericardial fluid	132	1.0	99.0
	Peritonial fluid	101	28.6	71.4

25 a Specimens tested from February 1994 to January 1995.

Table 5. Bacterial species (66) used for testing the specificity of DNA fragment probes, oligonucleotide probes and PCR primers.

	Bacterial species	Number of strains tested	Bacterial species	Number of strains tested
10	Gram negative:		Gram negative:	
	<i>Proteus mirabilis</i>	5	<i>Haemophilus parainfluenzae</i>	2
15	<i>Klebsiella pneumoniae</i>	5	<i>Bordetella pertussis</i>	2
	<i>Pseudomonas aeruginosa</i>	5	<i>Haemophilus parahaemolyticus</i>	2
	<i>Escherichia coli</i>	5	<i>Haemophilus haemolyticus</i>	2
	<i>Moraxella catarrhalis</i>	5	<i>Haemophilus aegyptius</i>	1
	<i>Proteus vulgaris</i>	2	<i>Kingella indologenes</i>	1
20	<i>Morganella morganii</i>	2	<i>Moraxella atlantae</i>	1
	<i>Enterobacter cloacae</i>	2	<i>Neisseria caviae</i>	1
	<i>Providencia stuartii</i>	1	<i>Neisseria subflava</i>	1
	<i>Providencia species</i>	1	<i>Moraxella urethralis</i>	1
	<i>Enterobacter agglomerans</i>	2	<i>Shigella sonnei</i>	1
25	<i>Providencia rettgeri</i>	2	<i>Shigella flexneri</i>	1
	<i>Neisseria mucosa</i>	1	<i>Klebsiella oxytoca</i>	2
	<i>Providencia alcalifaciens</i>	1	<i>Serratia marcescens</i>	2
	<i>Providencia rustigianii</i>	1	<i>Salmonella typhimurium</i>	1
	<i>Burkholderia cepacia</i>	2	<i>Yersinia enterocolitica</i>	1
30	<i>Enterobacter aerogenes</i>	2	<i>Acinetobacter calcoaceticus</i>	1
	<i>Stenotrophomonas maltophilia</i>	2	<i>Acinetobacter lwoffi</i>	1
	<i>Pseudomonas fluorescens</i>	1	<i>Hafnia alvei</i>	2
	<i>Comamonas acidovorans</i>	2	<i>Citrobacter diversus</i>	1
	<i>Pseudomonas putida</i>	2	<i>Citrobacter freundii</i>	1
35	<i>Haemophilus influenzae</i>	5	<i>Salmonella species</i>	1

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Table 5 (continued). Bacterial species (66) used for testing the specificity of DNA fragment probes,
 5 oligonucleotide probes and PCR primers.

	Bacterial species	Number of strains tested
10		
Gram positive:		
	<i>Streptococcus pneumoniae</i>	7
15	<i>Streptococcus salivarius</i>	2
	<i>Streptococcus viridans</i>	2
	<i>Streptococcus pyogenes</i>	2
	<i>Staphylococcus aureus</i>	2
	<i>Staphylococcus epidermidis</i>	2
20	<i>Staphylococcus saprophyticus</i>	5
	<i>Micrococcus species</i>	2
	<i>Corynebacterium species</i>	2
	<i>Streptococcus groupe B</i>	2
	<i>Staphylococcus simulans</i>	2
25	<i>Staphylococcus ludgunensis</i>	2
	<i>Staphylococcus capitis</i>	2
	<i>Staphylococcus haemolyticus</i>	2
	<i>Staphylococcus hominis</i>	2
	<i>Enterococcus faecalis</i>	2
30	<i>Enterococcus faecium</i>	1
	<i>Staphylococcus warneri</i>	1
	<i>Enterococcus durans</i>	1
	<i>Streptococcus bovis</i>	1
	<i>Diphtheroids</i>	1
35	<i>Lactobacillus acidophilus</i>	1

Table 6. Species-specific DNA fragment and oligonucleotide probes for hybridization.

5

Organisms ^a	Number of fragment probes ^b			Number of oligonucleotide probes		
	Tested	Specific	Ubiquitous ^c	Synthe-	Specific	Ubiqui-
				sized		tous ^c
<i>E. coli</i> ^d	-	-	-	20	12	9 ^f
<i>E. coli</i>	14	2	2 ^e	-	-	-
<i>K. pneumoniae</i> ^d	-	-	-	15	1	1
<i>K. pneumoniae</i>	33	3	3	18	12	8
<i>P. mirabilis</i> ^d	-	-	-	3	3	2
<i>P. mirabilis</i>	14	3	3 ^e	15	8	7
<i>P. aeruginosa</i> ^d	-	-	-	26	13	9
<i>P. aeruginosa</i>	6	2	2 ^e	6	0	0
<i>S. saprophyticus</i>	7	4	4	20	9	7
<i>H. influenzae</i> ^d	-	-	-	16	2	2
<i>H. influenzae</i>	1	1	1	20	1	1
<i>S. pneumoniae</i> ^d	-	-	-	6	1	1
<i>S. pneumoniae</i>	19	2	2	4	1	1
<i>M. catarrhalis</i>	2	2	2	9	8	8
<i>S. epidermidis</i>	62	1	1	-	-	-
<i>S. aureus</i>	30	1	1	-	-	-
Universal probes ^d	-	-	-	7	-	79

^a No DNA fragment or oligonucleotide probes were tested for *E. faecalis* and *S. pyogenes*.

^b Sizes of DNA fragments range from 0.25 to 5.0 kbp.

^c A specific probe was considered ubiquitous when at least 80% of isolates of the target species (approximately 80 isolates) were recognized by each specific probe. When 2 or more probes are combined, 100% of the isolates are recognized.

^d These sequences were selected from data banks.

^e Ubiquity tested with approximately 10 isolates of the target species.

^f A majority of probes (8/9) do not discriminate *E. coli* and *Shigella spp.*

^g Ubiquity tests with a pool of the 7 probes detected all 66 bacterial species listed in Table 5.

Table 7. PCR amplification for bacterial pathogens commonly encountered in urine, sputum, blood, cerebrospinal fluid and other specimens.

Organism	Primer pair ^a # (SEQ ID NO)	Amplicon size (bp)	Ubiquity ^b	DNA amplification from		
				colonies ^c	specimens ^d	
<i>E. coli</i>	1 ^e 2 ^e 3 4	(55+56) (46+47) (42+43) (131+132)	107 297 102 134	75/80 77/80 78/80 73/80	+	+
	1+3+4	-	80/80	+	+	
<i>E. faecalis</i>	1 ^e 2 ^e 1+2	(38+39) (40+41) -	200 121 80/80	71/80 79/80 79/80	+	+
<i>K. pneumoniae</i>	1 2 3 ^h 4 1+2+3	(67+68) (61+62) (135+136) (137+138) -	198 143 148 116 80/80	76/80 67/80 78/80 69/80 80/80	+	+
<i>P. mirabilis</i>	1 2	(74+75) (133+134)	167 123	73/80 80/80	+	N.T.
						N.T.
<i>P. aeruginosa</i>	1 ^e 2 ^e	(83+84) (85+86)	139 223	79/80 80/80	+	N.T.
						N.T.
<i>S. saprophyticus</i>	1 2	(98+99) (139+140)	126 190	79/80 80/80	+	+
						N.T.
<i>H. catarrhalis</i>	1 2 3	(112+113) (118+119) (160+119)	157 118 137	79/80 80/80 80/80	+	N.T.
						N.T.
						N.T.
<i>H. influenzae</i>	1 ^e	(154+155)	217	80/80	+	N.T.
<i>S. pneumoniae</i>	1 ^e 2 ^e 3	(156+157) (158+159) (78+79)	134 197 175	80/80 74/80 67/80	+	N.T.

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Table 7 (continued). PCR amplification for bacterial pathogens commonly encountered in urine, sputum, blood, 5 cerebrospinal fluid and other specimens.

Organism	Primer pair ^a (SEQ ID NO)	Amplicon size (bp)	Ubiquity ^b	DNA amplification from	
				colonies ^c	specimens ^d
<i>S. epidermidis</i>	1 (147+148)	175	80/80	+	N.T.
	2 (145+146)	125	80/80	+	N.T.
<i>S. aureus</i>	1 (152+153)	108	80/80	+	N.T.
	2 (149+150)	151	80/80	+	N.T.
	3 (149+151)	176	80/80	+	N.T.
<i>S. pyogenes</i> ^f	1 ^e (141+142)	213	80/80	+	N.T.
	2 ^e (143+144)	157	24/24	+	N.T.
Universal	1 ^e (126-127)	241	194/195 ^g	+	+

^a All primer pairs are specific in PCR assays since no amplification was observed with DNA from 66 different species of both Gram positive and Gram negative bacteria other than the species of interest (Table 5).

^b The ubiquity was normally tested on 80 strains of the species of interest. All retained primer pairs amplified at least 90% of the isolates. When combinations of primers were used, an ubiquity of 100% was reached.

^c For all primer pairs and multiplex combinations, PCR amplifications directly performed from a bacterial colony were 100 % species-specific.

^d PCR assays performed directly from urine specimens.

^e primer pairs derived from data bank sequences. Primer pairs with no "e" are derived from our species-specific fragments.

^f For *S. pyogenes*, primer pair #1 is specific for Group A Streptococci (GAS). Primer pair #2 is specific for the GAS-producing exotoxin A gene (*SpeA*).

^g Ubiquity tested on 195 isolates from 23 species representative of bacterial pathogens commonly encountered in clinical specimens.

^h Optimizations are in progress to eliminate non-specific amplification observed with some bacterial species other than the target species.

ⁱ N.T.: not tested.

Table 8. Selected antibiotic resistance genes for diagnostic purposes.

5

	Genes	Antibiotics	Bacteria ^a	SEQ ID NO
10	(bla _{tem}) TEM-1	β-lactams	Enterobacteriaceae, Pseudomonadaceae, Haemophilus, Neisseria	161
	(bla _{rob}) ROB-1	β-lactams	Haemophilus, Pasteurella	162
	(bla _{shv}) SHV-1	β-lactams	Klebsiella and other Enterobacteriaceae	163
15	aadB, aacC1, aacC2, aacC3, aacA	Aminoglycosides	Enterobacteriaceae, Pseudomonadaceae	164, 165, 166 167, 168
	mecA	β-lactams	Staphylococci	169
	vanH, vanA, vanX	Vancomycin	Enterococci	170
	satA	Macrolides	Enterococci	173
	aacA-aphD	Aminoglycosides	Enterococci, Staphylococci	174
	vat	Macrolides	Staphylococci	175
20	vga	Macrolides	Staphylococci	176
	msrA	Erythromycin	Staphylococci	177
	Int and Sul conserved sequences	β-lactams, trimethoprim, aminoglycosides, anti-, septic, chloramphenicol	Enterobacteriaceae, Pseudomonadaceae	171, 172

30 ^a Bacteria having high incidence for the specified antibiotic resistance genes. The presence in other bacteria is not excluded.

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**Annex I: Specific and ubiquitous oligonucleotides
probes for hybridization**

5	SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
			SEQ ID NO	Nucleotide position
10				
		<u>Bacterial species: Escherichia coli</u>		
	44	5'-CAC CCG CTT GCG TGG CAA GCT GCC C	5 ^a	213-237
	45	5'-CGT TTG TGG ATT CCA GTT CCA TCC G	5 ^a	489-513
	48	5'-TGA AGC ACT GGC CGA AAT GCT GCG T	6 ^a	759-783
15	49	5'-GAT GTA CAG GAT TCG TTG AAG GCT T	6 ^a	898-922
	50	5'-TAG CGA AGG CGT AGC AGA AAC TAA C	7 ^a	1264-1288
	51	5'-GCA ACC CGA ACT CAA CGC CGG ATT T	7 ^a	1227-1251
	52	5'-ATA CAC AAG GGT CGC ATC TGC GGC C	7 ^a	1313-1337
	53	5'-TGC GTA TGC ATT GCA GAC CTT GTG GC	7 ^a	111-136
20	54	5'-GCT TTC ACT GGA TAT CGC GCT TGG G	7 ^a	373-397
		<u>Bacterial species: Proteus mirabilis</u>		
	70 ^b	5'-TGG TTC ACT GAC TTT GCG ATG TTT C	12	23-47
	71	5'-TCG AGG ATG GCA TGC ACT AGA AAA T	12	53-77
25	72 ^b	5'-CGC TGA TTA GGT TTC GCT AAA ATC TTA TTA	12	80-109
	73	5'-TTG ATC CTC ATT TTA TTA ATC ACA TGA CCA	12	174-203

^a Sequences from data banks

^b These sequences are from the opposite DNA strand of the

30 sequences given in the Sequence listing

**Annex I: Specific and ubiquitous oligonucleotides
probes for hybridization**

5	SEQ ID NO	Nucleotide sequence	Originating DNA fragment		
			SEQ ID NO	Nucleotide position	
10	<u>Bacterial species:</u> <i>Proteus mirabilis</i>				
	76	5'-CCG CCT TTA GCA TTA ATT GGT GTT TAT AGT	13	246-275	
	77	5'-CCT ATT GCA GAT ACC TTA AAT GTC TTG GGC	13	291-320	
	80 ^b	5'-TTG AGT GAT GAT TTC ACT GAC TCC C	14	18-42	
	81	5'-GTC AGA CAG TGA TGC TGA CGA CAC A	15 ^a	1185-1209	
15	82	5'-TGG TTG TCA TGC TGT TTG TGT GAA AAT	15 ^a	1224-1250	
		<u>Bacterial species:</u> <i>Klebsiella pneumoniae</i>			
	57	5'-GTG GTG TCG TTC AGC GCT TTC AC	8	45-67	
	58	5'-GCG ATA TTC ACA CCC TAC GCA GCC A	9	161-185	
20	59 ^b	5'-GTC GAA AAT GCC GGA AGA GGT ATA CG	9	203-228	
	60 ^b	5'-ACT GAG CTG CAG ACC GGT AAA ACT CA	9	233-258	
	63 ^b	5'-CGT GAT GGA TAT TCT TAA CGA AGG GC	10	250-275	
	64 ^b	5'-ACC AAA CTG TTG AGC CGC CTG GA	10	201-223	
	65	5'-GTG ATC GCC CCT CAT CTG CTA CT	10	77-99	
25	66	5'-CGC CCT TCG TTA AGA ATA TCC ATC AC	10	249-274	
	69	5'-CAG GAA GAT GCT GCA CCG GTT GTT G	11 ^a	296-320	

^a Sequences from data banks

^b These sequences are from the opposite DNA strand of the
30 sequences given in the Sequence listing

**Annex I: Specific and ubiquitous oligonucleotides
probes for hybridization**

5	SEQ ID NO	Nucleotide sequence	Originating DNA fragment		
			SEQ ID NO	Nucleotide position	
10	<u>Bacterial species:</u> <i>Pseudomonas aeruginosa</i>				
87	5'-AAT GCG GCT GTA CCT CGG CGC TGG T	18 ^a	2985-3009		
88	5'-GGC GGA GGG CCA GTT GCA CCT GCC A	18 ^a	2929-2953		
89	5'-AGC CCT GCT CCT CGG CAG CCT CTG C	18 ^a	2821-2845		
90	5'-TGG CTT TTG CAA CCG CGT TCA GGT T	18 ^a	1079-1103		
15	5'-GCG CCC GCG AGG GCA TGC TTC GAT G	19 ^a	705-729		
91	5'-ACC TGG GCG CCA ACT ACA AGT TCT A	19 ^a	668-692		
92	5'-GGC TAC GCT GCC GGG CTG CAG GCC G	19 ^a	505-529		
93	5'-CCG ATC TAC ACC ATC GAG ATG GGC G	20 ^a	1211-1235		
94	5'-GAG CGC GGC TAT GTG TTC GTC GGC T	20 ^a	2111-2135		
20	<u>Bacterial species:</u> <i>Streptococcus pneumoniae</i>				
120	5'-TCT GTG CTA GAG ACT GCC CCA TTT C	30	423-447		
121	5'-CGA TGT CTT GAT TGA GCA GGG TTA T	31 ^a	1198-1222		
25	<u>a</u> Sequences from data banks				
	<u>b</u> These sequences are from the opposite DNA strand of the sequences given in the Sequence listing				

**Annex I: Specific and ubiquitous oligonucleotides
probes for hybridization**

5	SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
			SEQ ID NO	Nucleotide position
10		Bacterial species: <i>Staphylococcus saprophyticus</i>		
	96	5'-CGT TTT TAC CCT TAC CTT TTC GTA CTA CC	21	45-73
	97 ^b	5'-TCA GGC AGA GGT AGT ACG AAA AGG TAA GGG	21	53-82
	100	5'-CAC CAA GTT TGA CAC GTG AAG ATT CAT	22	89-115
	101 ^b	5'-ATG AGT GAA GCG GAG TCA GAT TAT GTG CAG	23	105-134
15	102	5'-CGC TCA TTA CGT ACA GTG ACA ATC G	24	20-44
	103	5'-CTG GTT AGC TTG ACT CTT AAC AAT CTT GTC	24	61-90
	104 ^b	5'-GAC GCG ATT GTC ACT GTA CGT AAT GAG CGA	24	19-48
		Bacterial species: <i>Moraxella catarrhalis</i>		
20	108	5'-GCC CCA AAA CAA TGA AAC ATA TGG T	28	81-105
	109	5'-CTG CAG ATT TTG GAA TCA TAT CGC C	28	126-150
	110	5'-TGG TTT GAC CAG TAT TTA ACG CCA T	28	165-189
	111	5'-CAA CGG CAC CTG ATG TAC CTT GTA C	28	232-256
	114	5'-TTA CAA CCT GCA CCA CAA GTC ATC A	29	97-121
25	115	5'-GTA CAA ACA AGC CGT CAG CGA CTT A	29	139-163
	116	5'-CAA TCT GCG TTG GTG CGT TCA CT	29	178-200
	117	5'-GCT ACT TTG TCA GCT TTA GCC ATT CA	29	287-312
<hr/> <p>^a Sequences from data banks</p>				
30	^b	These sequences are from the opposite DNA strand of the sequences given in the Sequence listing		

**Annex I: Specific and ubiquitous oligonucleotides
probes for hybridization**

5	SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
			SEQ ID NO	Nucleotide position
10	Bacterial species: <i>Haemophilus influenzae</i>			
	105 ^b	5'-GCG TCA GAA AAA GTA GGC GAA ATG AAA G	25	138-165
	106 ^b	5'-AGC GGC TCT ATC TTG TAA TGA CAC A	26 ^a	770-794
	107 ^b	5'-GAA ACG TGA ACT CCC CTC TAT ATA A	27 ^a	5184-5208
15	Universal probes^c			
	122 ^b	5'-ATC CCA CCT TAG GCG GCT GGC TCC A	-	-
	123	5'-ACG TCA AGT CAT CAT GGC CCT TAC GAG TAG G	-	-
	124 ^b	5'-GTG TGA CGG GCG GTG TGT ACA AGG C	-	-
	125 ^b	5'-GAG TTG CAG ACT CCA ATC CGG ACT ACG A	-	-
20	128 ^b	5'-CCC TAT ACA TCA CCT TGC GGT TTA GCA GAG AG	-	-
	129	5'-GGG GGG ACC ATC CTC CAA GGC TAA ATA C	-	-
	130 ^b	5'-CGT CCA CTT TCG TGT TTG CAG AGT GCT GTG TT	-	-

^a Sequences from data banks

^b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

^c Universal probes were derived from 16S or 23S ribosomal RNA gene sequences not included in the Sequence listing

Annex II: Specific and ubiquitous primers for DNA amplification

5	SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
			SEQ ID NO	Nucleotide position
10	<u>Bacterial species:</u>	<i>Escherichia coli</i>		
	42	5'-GCT TTC CAG CGT CAT ATT G	4	177-195
	43 ^b	5'-GAT CTC GAC AAA ATG GTG A	4	260-278
	46	5'-TCA CCC GCT TGC GTG GC	5 ^a	212-228
	47 ^b	5'-GGA ACT GGA ATC CAC AAA C	5 ^a	490-508
15	55	5'-GCA ACC CGA ACT CAA CGC C	7 ^a	1227-1245
	56 ^b	5'-GCA GAT GCG ACC CTT GTG T	7 ^a	1315-1333
	131	5'-CAG GAG TAC GGT GAT TTT TA	3	60-79
	132 ^b	5'-ATT TCT GGT TTG GTC ATA CA	3	174-193
20	<u>Bacterial species:</u>	<i>Enterococcus faecalis</i>		
	38	5'-GCA ATA CAG GGA AAA ATG TC	1 ^a	69-88
	39 ^b	5'-CTT CAT CAA ACA ATT AAC TC	1 ^a	249-268
	40	5'-GAA CAG AAG AAG CCA AAA AA	2 ^a	569-588
	41 ^b	5'-GCA ATC CCA AAT AAT ACG GT	2 ^a	670-689
25				

^a Sequences from data banks

^b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

Annex II: Specific and ubiquitous primers for DNA amplification

5	SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
			SEQ ID NO	Nucleotide position
10				
		<u>Bacterial species:</u> <i>Klebsiella pneumoniae</i>		
	61	5'-GAC AGT CAG TTC GTC AGC C	9	37-55
	62 ^b	5'-CGT AGG GTG TGA ATA TCG C	9	161-179
	67	5'-TCG CCC CTC ATC TGC TAC T	10	81-99
15	68 ^b	5'-GAT CGT GAT GGA TAT TCT T	10	260-278
	135	5'-GCA GCG TGG TGT CGT TCA	8	40-57
	136 ^b	5'-AGC TGG CAA CGG CTG GTC	8	170-187
	137	5'-ATT CAC ACC CTA CGC AGC CA	9	166-185
	138 ^b	5'-ATC CGG CAG CAT CTC TTT GT	9	262-281
20				
		<u>Bacterial species:</u> <i>Proteus mirabilis</i>		
	74	5'-GAA ACA TCG CAA AGT CAG T	12	23-41
	75 ^b	5'-ATA AAA TGA GGA TCA AGT TC	12	170-189
	133	5'-CGG GAG TCA GTG AAA TCA TC	14	17-36
25	134 ^b	5'-CTA AAA TCG CCA CAC CTC TT	14	120-139

^a Sequences from data banks

^b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

Annex II: Specific and ubiquitous primers for DNA amplification

5	SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
			SEQ ID NO	Nucleotide position
10	<u>Bacterial species:</u> <i>Staphylococcus saprophyticus</i>			
	98	5'-CGT TTT TAC CCT TAC CTT TTC GTA CT	21	45-70
	99 ^b	5'-ATC GAT CAT CAC ATT CCA TTT GTT TTT A	21	143-170
	139	5'-CTG GTT AGC TTG ACT CTT AAC AAT C	24	61-85
	140 ^b	5'-TCT TAA CGA TAG AAT GGA GCA ACT G	24	226-250
15	<u>Bacterial species:</u> <i>Pseudomonas aeruginosa</i>			
	83	5'-CGA GCG GGT GGT GTT CAT C	16 ^a	554-572
	84 ^b	5'-CAA GTC GTC GTC GGA GGG A	16 ^a	674-692
	85	5'-TCG CTG TTC ATC AAG ACC C	17 ^a	1423-1441
20	86 ^b	5'-CCG AGA ACC AGA CTT CAT C	17 ^a	1627-1645
	<u>Bacterial species:</u> <i>Moraxella catarrhalis</i>			
	112	5'-GGC ACC TGA TGT ACC TTG	28	235-252
	113 ^b	5'-AAC AGC TCA CAC GCA TT	28	375-391
25	118	5'-TGT TTT GAG CTT TTT ATT TTT TGA	29	41-64
	119 ^b	5'-CGC TGA CGG CTT GTT TGT ACC A	29	137-158
	160	5'-GCT CAA ATC AGG GTC AGC	29	22-39
	119 ^b	5'-CGC TGA CGG CTT GTT TGT ACC A	29	137-158
30	^a Sequences from data banks			
	^b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing			

Annex II: Specific and ubiquitous primers for DNA amplification

5	SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
			SEQ ID NO	Nucleotide position
10	<u>Bacterial species:</u> <i>Staphylococcus epidermidis</i>			
	145	5'-ATC AAA AAG TTG GCG AAC CTT TTC A	36	21-45
	146 ^b	5'-CAA AAG AGC GTG GAG AAA AGT ATC A	36	121-145
	147	5'-TCT CTT TTA ATT TCA TCT TCA ATT CCA TAG	36	448-477
	148 ^b	5'-AAA CAC AAT TAC AGT CTG GTT ATC CAT ATC	36	593-622
15	<u>Bacterial species:</u> <i>Staphylococcus aureus</i>			
	149 ^b	5'-CTT CAT TTT ACG GTG ACT TCT TAG AAG ATT	37	409-438
	150	5'-TCA ACT GTA GCT TCT TTA TCC ATA CGT TGA	37	288-317
	149 ^b	5'-CTT CAT TTT ACG GTG ACT TCT TAG AAG ATT	37	409-438
20	151	5'-ATA TTT TAG CTT TTC AGT TTC TAT ATC AAC	37	263-292
	152	5'-AAT CTT TGT CGG TAC ACG ATA TTC TTC ACG	37	5-34
	153 ^b	5'-CGT AAT GAG ATT TCA GTA GAT AAT ACA ACA	37	83-112
25	a	Sequences from data banks		
	b	These sequences are from the opposite DNA strand of the sequences given in the Sequence listing		

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Annex II: Specific and ubiquitous primers for DNA amplification

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	SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
			SEQ ID NO	Nucleotide position
10				
		<u>Bacterial species:</u> <i>Haemophilus influenzae</i>		
	154	5'-TTT AAC GAT CCT TTT ACT CCT TTT G	27a	5074-5098
	155b	5'-ACT GCT GTT GTA AAG AGG TTA AAA T	27a	5266-5290
15				
		<u>Bacterial species:</u> <i>Streptococcus pneumoniae</i>		
	78	5'-AGT AAA ATG AAA TAA GAA CAG GAC AG	34	164-189
	79b	5'-AAA ACA GGA TAG GAG AAC GGG AAA A	34	314-338
	156	5'-ATT TGG TGA CGG GTG ACT TT	31a	1401-1420
	157b	5'-GCT GAG GAT TTG TTC TTC TT	31a	1515-1534
20	158	5'-GAG CGG TTT CTA TGA TTG TA	35a	1342-1361
	159b	5'-ATC TTT CCT TTC TTG TTC TT	35a	1519-1538
		<u>Bacterial species:</u> <i>Streptococcus pyogenes</i>		
	141	5'-TGA AAA TTC TTG TAA CAG GC	32a	286-305
25	142b	5'-GGC CAC CAG CTT GCC CAA TA	32a	479-498
	143	5'-ATA TTT TCT TTA TGA GGG TG	33a	966-985
	144b	5'-ATC CTT AAA TAA AGT TGC CA	33a	1103-1122

a Sequences from data banks
 30 b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

Annex II: Specific and ubiquitous primers for DNA amplification

5	SEQ ID NO	Nucleotide sequence	Originating DNA fragment	
			SEQ ID NO	Nucleotide position
Universal primers^c				
10	126	5'-GGA GGA AGG TGG GGA TGA CG	-	-
	127 ^b	5'-ATG GTG TGA CGG GCG GTG TG	-	-

^a Sequences from data banks

15 ^b These sequences are from the opposite DNA strand of the sequences given in the Sequence listing

^c Universal primers were derived from the 16S ribosomal RNA gene sequence not included in the Sequence listing

Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.

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Reverse strand of SEQ ID NO: 122

TGGAGCC AGCCGCTAA CGTGGGAT

10	1461	1510
<i>Streptococcus salivarius</i>	TGAGGTAACC	TTTGGAGCC
<i>Proteus vulgaris</i>	TAGCTTAACC	AGCCGCTAA
<i>Pseudomonas aeruginosa</i>	TAGCTTAACC	CGTGGGAT
<i>Neisseria gonorrhoeae</i>	TAGGTTAAC	ATGAACTGGGG
<i>Streptococcus lactis</i>	TTGCCTAAC	TGAGCTTTC

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Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.

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	SEQ ID NO.:	ACGTCAAGTC	ATCATGGC CCTTACGAT AGG
	1251		1300
10	<i>Haemophilus influenzae</i>	GGTNGGGATG	ATCATGGC CCTTACGAT AGGCTACAC
	<i>Neisseria gonorrhoeae</i>	GGTGGGGATG	CTCATGGC CCTTATGAC CAGGCTTCAC
	<i>Pseudomonas cepacia</i>	GGTNGGGATG	CTCATGGC CCTTATGAT AGGCTTCAC
	<i>Serratia marcescens</i>	GGTGGGGATG	CTCATGGC CCTTATGAT AGGCTTCAC
	<i>Escherichia coli</i>	GGTGGGGATG	ATCATGGC CCTTACGAC CAGGCTACAC
	<i>Proteus vulgaris</i>	GGTGGGGATG	ATCATGGC CCTTACGAT AGGCTACAC
	<i>Pseudomonas aeruginosa</i>	GGTGGGGATG	ATCATGGC CCTTACGAT AGGCTACAC
	<i>Clostridium perfringens</i>	GGTGGGGATG	ATCATGGC CNTTATGAT AGGCTACAC
	<i>Mycoplasma hominis</i>	GGTGGGGATG	ATCATGGC TCTTACGAT GAGGCCACAC
	<i>Helicobacter pylori</i>	GGTGGGGACG	ATCATGGC CCTTACGAT AGGCTACAC
15	<i>Mycoplasma pneumoniae</i>	GGAAGGGATG	ATCATGGC CCTTATGCT AGGCTGCAA
20			

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Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.

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Reverse of the probe SEQ ID NO: 124	149
cccttttaca cccccccat caccac	1451
Escherichia coli	ACGTTCCGG
Neisseria gonorrhoeae	ACGTTCCNG
Pseudomonas cepacia	ACGTTCCGG
Serratia marcescens	ACGTTCCGG
Proteus vulgaris	ACGTTCCGG
Haemophilus influenzae	ACGTTCCGG
Pseudomonas aeruginosa	ACGTTCCGG
Clostridium perfringens	ACGTTCCNG
Mycoplasma hominis	ACGTTCTCGG
Helicobacter pylori	ACGTTCCGG
Mycoplasma pneumoniae	ACGTTCTCGG

Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.

Reverse strand of SEQ ID NO 125: TCG TAGTCCGGAT TGGAGTCTGCC AACTC

10	<i>Escherichia coli</i>	AAGTGGTCC	TAGTCCGGAT	TGAGTCTGC	AACTGACTC
	<i>Neisseria gonorrhoeae</i>	AAACCGATCC	TAATCCGGAT	TGCACTCTGC	AACTGGAGTC
	<i>Pseudomonas cepacia</i>	AAACCGATCC	TAATCCGGAT	TGCACTCTGC	AACTGGAGTC
	<i>Serratia marcescens</i>	AAGTATGTC	TAATCCGGAT	TGAGTCTGC	AACTGACTC
	<i>Proteus vulgaris</i>	AAGTCTGTC	TAATCCGGAT	TGAGTCTGC	AACTGACTC
	<i>Haemophilus influenzae</i>	AAGTACGTC	AAATCCGGAT	TGAGTCTGC	AACTGACTC
	<i>Pseudomonas aeruginosa</i>	AAACCGATCC	TAATCCGGAT	CGCACTCTGC	AACTGGAGTC
	<i>Clostridium perfringens</i>	AAACCAAGTC	CAATTCCGGAT	TGAGGCTCA	AACTGGCTCA
	<i>Mycoplasma hominis</i>	AAGCCGATCT	CAATTCCGGAT	TGAGTCTGC	AAATTGACTC
	<i>Helicobacter pylori</i>	ACACC..TCT	CAATTCCGGAT	TGAGGCTCA	AACTGGCTCG
15	<i>Mycoplasma pneumoniae</i>	AAATTGGTC	CAATTCCGGAT	TGAGGCTCA	AAATTGTCCT

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Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.

5

Reverse strand of SEQ ID NO: 128 CT CTCCTCAA CGCCAGCT ATGATAGG

10	<i>Lactobacillus lactis</i>	AAACACAGCT CTCCTCAA CGCCAGCT ATGATAGG CGTGACGGCT
	<i>Escherichia coli</i>	AAACACAGCA CTGCTCAAAC AGCAAGCTG AGCTATACGG TGTGACGGCT
	<i>Pseudomonas aeruginosa</i>	AAACACAGCA CTGCTCAAAC AGCAAGCTG AGCTATACGG TGTGACGGCT
15	<i>Pseudomonas cepacia</i>	AAACACAGCA CTGCTCAAAC AGCAAGCTG AGCTATACGG TGTGACGGCT
	<i>Bacillus stearothermophilus</i>	AAACACAGGT CTGCTCAAAG TCCTAAAGG AGCTATACGG GCTGACACCT
	<i>Micrococcus luteus</i>	AAACACAGGT CTGCTCAAAG TCCTAAAGG ATGATATGG ACTGACTCTT

SEQ ID NO: 129

1991	GGGGGACCC ATCCCTCAA CGCTAAATAC	530
20	<i>Escherichia coli</i>	TGTCTGAATA TGGGGGACCC ATCCCTCAA CGCTAAATAC CCTGACTGAC
	<i>Pseudomonas aeruginosa</i>	TGTCTGAACA TGGGGGACCC ATCCCTCAA CGCTAAATAC ACTGACTGAC
	<i>Pseudomonas cepacia</i>	TGTCTGAAGA TGGGGGACCC ATCCCTCAA CGCTAAATAC CGTGATCGAC
20	<i>Lactobacillus lactis</i>	AGTTTGAAATC CGGGAGGACC ATCTCCAAAC CCTAAATACCT CCTTAGTGAC
	<i>Micrococcus luteus</i>	CGTGTGAATC TGGCAAGGACCC ACCTGGTAA CGCTAAATAC ACCTGTTGAC

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Annex III. Selection of universal probes by alignment of the sequences of bacterial 16S and 23S ribosomal RNA genes.

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	Reverse strand of SEQ ID NO: 130	1981	2030
10	<i>Pseudomonas aeruginosa</i>	TGTTTATCAA	AAACACAGCA CTCTGCAAC ACGAAAGCTGG ACGTATAGGG
	<i>Escherichia coli</i>	TGTTTATCAA	AAACACAGCA CTGTGCAAC ACGAAAGCTGG ACGTATACGG
	<i>Pseudomonas cepacia</i>	TGTTTATCAA	AAACACAGCA CTCTGCAAC ACGAAAGCTGG ACGTATAGGG
	<i>Bacillus stearothermophilus</i>	TGTTTATCAA	AAACACAGGT CTCTGGAAAG TCGTAAAGGG ACGTATAGGG
	<i>Lactobacillus lactis</i>	TGTTTATCAA	AAACACAGCT CTCTGCTAAA CGGCAAGGTG ATGTATAGGG
15	<i>Micrococcus luteus</i>	TGTTTATCAA	AAACACAGGT CCATGCGAAG TCGTAAAGACG ATGTATATGG

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Annex IV. Selection of the universal PCR primers by alignment of the bacterial 16S ribosomal RNA gene

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: BERGERON, Michel G.
OUELLETTE, Marc
ROY, Paul H.

(ii) TITLE OF THE INVENTION: SPECIFIC AND UNIVERSAL PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN MICROBIOLOGY LABORATORIES

(iii) NUMBER OF SEQUENCES: 177

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE:
(B) STREET:
(C) CITY:
(D) STATE:
(E) COUNTRY:
(F) ZIP:

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: FLOPPY DISK, 800K
(B) COMPUTER: Macintosh IIci
(C) OPERATING: System 7.0
(D) SOFTWARE: Word 5.1a

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION;

(A) NAME: JEAN C. BAKER
(B) REGISTRATION NUMBER:

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE:
(B) TELEFAX:

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1817 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACAGTAAAAA	AGTTGTTAAC	GAATGAATT	GTTAACAACT	TTTTGCTAT	50
GGTATTGAGT	TATGAGGGGC	AATACAGGGA	AAAATGTCGG	CTGATTAAGG	100
AATTTAGATA	GTGCCGGTTA	GTAGTTGTCT	ATAATGAAAA	TAGCAACAAA	150
TATTTACGCA	GGGAAAGGGG	CGGTCGTTA	ACGGGAAAAA	TTAGGGAGGA	200
TAAAGCAATA	CTTTGTTGG	GAAAAGAAAAT	AAAAGGAAAC	TGGGGAAAGGA	250
GTAAATTGTT	TGATGAAGGG	AAATAAAATT	TTATACATT	TAGGTACAGG	300
CATCTTGT	GGAAGTCAT	GTCTATTTTC	TTCACTTTT	GTAGCCGCAG	350
AAGAACAAAGT	TTATTCAAGAA	AGTGAAGTTT	CAACAGTTT	ATCGAAGTTG	400
GAAAAGGAGG	CAATTCTGA	GGCAGCTGCT	GAACAATATA	CGGTTGTTAGA	450
TCGAAAAGAA	GACGCGTGGG	GGATGAAGCA	TCTTAAGTTA	GAAAAGCAAA	500
CGGAAGGCCT	TACTGTTGAT	TCAGATAATG	TGATTATTCA	TTTAGATAAA	550
AACGGTGCAG	TAACAAGTGT	TACAGGAAAT	CCAGTTGATC	AAGTTGTGAA	600
AATTCAATCG	GTTGATGCAA	TCGGTGAAGA	AGGAGTTAAA	AAAATTGTTG	650
CTTCTGATAA	TCCAGAAACT	AAAGATCTG	TCTTTTTAGC	TATTGACAAA	700
CGTGTAAATA	ATGAAGGGCA	ATTATTTTAT	AAAGTCAGAG	TAACCTCTTC	750
ACCAACTGGT	GACCCGTAT	CATTGGTTA	TAAAGTGAAC	GCTACAGATG	800
GAACAATTAT	GGAAAAACAA	GATTTAACGG	AACATGTCGG	TAGTGAAGTA	850
ACGTTAAAAA	ACTCTTTCA	AGTAACGTTT	AATGTACCAAG	TTGAAAAAAG	900
CAATACGGGA	ATTGCTTTAC	ACGGAACGGA	TAACACAGGG	GTTCACCATG	950
CAGTAGTTGA	TGGCAAAAT	AATTATTCTA	TTATTCAAGC	GCCATCACTA	1000
GCGACATTAA	ATCAGAATGC	TATTGACGCC	TATACGCATG	GAAAATTGT	1050
GAAAACATAT	TATGAAGATC	ATTTCCAACG	ACACAGTATT	GATGATCGAG	1100
GGATGCCCAT	CTTGTCAAGT	GTTGATGAAC	AACATCCAGA	TGCTTATGAC	1150
AATGCTTTT	GGGATGGAAA	AGCAATGCGT	TATGGTGAAA	CAAGTACACC	1200
AACAGGAAAA	ACGTATGCTT	CCTCTTTAGA	TGTAGTTGGT	CATGAAATGA	1250
CACATGGTGT	GACGGAACAT	ACTGCCGGTT	TAGAATATT	AGGACAATCA	1300
GGTGCCTTGA	ATGAATCTTA	TTCTGATTG	ATGGGTTATA	TTATTCGGG	1350

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TGCATCTAAT	CCAGAAATTG	GTGCGGATAC	TCAGAGTGT	GACCGAAAAA	1400
CAGGTATTCTG	AAATTTACAA	ACGCCAAGTA	AACACGGACA	ACCAGAAACC	1450
ATGGCTCAAT	ACGACGATCG	AGCACGGTAT	AAAGGAACGC	CTTATTATGA	1500
TCAAGGCGGT	GTTCATTTATA	ACAGTGGAAAT	TATTAATCGG	ATTGGTTACA	1550
CCATTATCCA	GAACCTAGGC	ATTGAAAAAG	CACAGACTAT	TTTCTACAGC	1600
TCGTTAGTAA	ATTACTTAAC	ACCTAAAGCA	CAATTCAAGTG	ATGCTCGTGC	1650
TGCGATGCTT	GCTGCTGCAA	AAGTTCAATA	TGGCGATGAA	GCAGCTTCAG	1700
TGGTGTCAAGC	AGCCTTTAAC	TCTGCTGGAA	TCGGAGCTAA	AGAAGACATT	1750
CAGGTAAACC	AACCAAGTGA	ATCTGTTCTG	GTCAATGAAT	AAAAAAAATT	1800
CCCCAATTAA	ATAAAAAA				1817

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2275 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGTACCAAAG	AAAAAAACGA	ACGCCACAAC	CAACAGCCTC	TAAAGCAACA	50
CCTGCTTCTG	AAATTGAGGG	AGATTAGCA	AATGTCAATG	AGATTCTTTT	100
GGTCACGAT	GATCGTGTG	GGTCAGCAAC	GATGGGAATG	AAAGTCTTAG	150
AAGAAATTCTT	AGATAAAAGAG	AAAATTCAA	TGCCGATTG	AAAAATTAAAT	200
ATTAATGAAT	TAACCAACA	AACACAGGCT	TTAATTGTCA	CAAAAGCTGA	250
ACTAACGGAA	CAAGCACGTA	AAAAGCACC	GAAAGCGACA	CACTTATCAG	300
TAAAAAGTTA	TGGTTAATCC	CCAAAAATAT	GAAACAGTGG	GTTTCGCTCT	350
TAAAAGAAAG	TGCCCTAGAGA	GGAAGAAAAC	AATGGAAAAT	CTTACGAATA	400
TTTCAATTGA	ATTAAATCAA	CAGTTAATA	CAAAAGAAGA	AGCTATTGCG	450
TTTTCCGGCC	AGAAACTAGT	CGAGGCAGGC	TGTGTTGAGC	CCGCTTATAT	500
CGAACGAAATG	ATTGAAAGAG	ACCAATTGCT	ATCTGCCAT	ATGGGGAAATT	550
TTATTGCCAT	TCCTCATGGA	ACAGAAGAAG	CCAAAAAATT	AGTAAAAAAA	600
TCAGGAATCT	GTGTAGTGCA	AGTCCCAGAG	GGCGTTAATT	TTGGCACCGA	650
AGAAGATGAA	AAAATTGCTA	CCGTATTATT	TGGGATTGCC	GGAGTCGGTG	700
AAGAACATTT	GCAATTAGTC	CAACAAATTG	CACTTTATTG	TAGTGATATG	750
GATAACGTGG	TGCAACTTGC	CGATGCATTA	AGTAAAGAAG	AAATAACAGA	800

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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GATCCGCCAT	GGGTTGTTTT	CCGATTGAGG	ATTTTATAGA	TGGTTCTGG	50
CGACCTGCAC	AGGAGTACGG	TGATTTTAA	TTATTGCAAT	TGCACAAGAG	100
TCAGTTCTCC	CCCAAAGACA	GCACCGGTAT	CAATATAATG	CAGGTTGCCA	150
ATATCCACGC	GATGGCGCAA	AGGTGTATGA	CCAAACCAGA	AATGATCGGC	200
CACCTGCATC	GCCAGTCGC	GAGTCGG			227

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GATCTAAATC	AAATTAATTG	GTTAAAGATA	ACACACAGCGG	GGCCGACATA	50
AACTCTGACA	AGAAGTTAAC	AACCATATAA	CCTGCACAGG	ACGCGAACAT	100
GTCTTCTCAT	CCGTATGTCA	CCCAGCAAAA	TACCCCGCTG	GCGGACGACA	150
CCACTCTGAT	GTCCCACTACC	GATCTCGCTT	TCCAGCGTCA	TATTGGGGCG	200
CGCTACGTTG	GGGCGTGGGC	GTAATTGGTC	AATCAGGCGC	GGGGTCAGCG	250
GATAAACATT	CACCATTTTG	TCGAGATC			278

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(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1596 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGGCTGACA	TTCTGCTGCT	CGATAATATC	GACTCTTTA	CGTACAACCT	50
GGCAGATCAG	TTGCGCAGCA	ATGGGCATAA	CGTGGTGATT	TACCGCAACC	100
ATATACCGGC	GCAAACCTTA	ATTGAACGCT	TGGCGACCAT	GAGTAATCCG	150
GTGCTGATGC	TTTCTCCTGG	CCCCGGTGTG	CCGAGCGAAG	CCGGTTGTAT	200
GCCGGAACTC	CTCACCCGCT	TGCGTGGCAA	GCTGCCATT	ATTGGCATT	250
GCCTCGGACA	TCAGGCGATT	GTCGAAGCTT	ACGGGGGCTA	TGTCGGTCAG	300
GCAGGGCGAAA	TTCTCCACGG	TAAAGCCTCC	AGCATTGAAC	ATGACGGTCA	350
GGCGATGTTT	GCCGGATTAA	CAAACCCGCT	GCCGGTGGCG	CGTTATCACT	400
CGCTGGTTGG	CAGTAACATT	CCGGCCGGTT	TAACCATCAA	CGCCCATT	450
AATGGCATGG	TGATGGCAGT	ACGTCACGAT	GGGGATCGCG	TTTGTGGATT	500
CCAGTTCCAT	CCGGAATCCA	TTCTCACCA	CCAGGGCGCT	CGCTGCTGG	550
AACAAACGCT	GGCCTGGCG	CAGCATAAAC	TAGAGCCAGC	CAACACGCTG	600
CAACCGATT	TGGAAAAACT	GTATCAGCG	CAGACGTTA	GCCAACAAGA	650
AAGCCACCAG	CTGTTTCAG	CGGTGGTGC	TGGCGAGCTG	AAGCCGGAAC	700
AACTGGCGGC	GGCGCTGGTG	AGCATGAAAA	TTCGCGGTGA	GCACCCGAAC	750
GAGATCGCCG	GGGCAGCAAC	CGCGCTACTG	GAAAACCGAG	CGCCGTTCCC	800
GCGCCCGGAT	TATCTGTTG	CTGATATCGT	CGGTACTGGC	GGTGACGGCA	850
GCAACAGTAT	CAATATTCT	ACCGCCAGTG	CGTTTGTGCG	CGCGGCCTGT	900
GGGCTGAAAG	TGGCGAAACA	CGGCAACCGT	AGCGTCTCCA	GTAAATCTGG	950
TTCGTCCGAT	CTGCTGGCGG	CGTTCGGTAT	TAATCTTGAT	ATGAACGCCC	1000
ATAAAATCGCG	CCAGGCGCTG	GATGAGTTAG	GTGTATGTTT	CCTCTTTGCG	1050
CCGAAGTATC	ACACCGGATT	CCGCCACGCG	ATGCCGGTTC	GCCAGCAACT	1100
GAAAACCCGC	ACCTGTTCA	ATGTGCTGGG	GCCATTGATT	AACCCGGCGC	1150
ATCCGCCGCT	GGCGTTAATT	GGTGTGTTATA	GTCCGGAACT	GGTGCTGCCG	1200
ATTGCCGAAA	CCTTGCGCGT	GCTGGGTAT	CAACGCGCGG	CGGTGGTGCA	1250
CAGCGGGCGG	ATGGATGAAG	TTTCATTACA	CGCGCCGACA	ATCGTTGCCG	1300
AACTGCATGA	CGGGCAAATT	AAAAGCTATC	AGCTCACCGC	AGAAGACTTT	1350

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GGCCTGACAC	CCTACCACCA	GGAGCAACTG	GCAGGGCGAA	CACCGGAAGA	1400
AAACCGTGAC	ATTTAACAC	GTTTGTACCA	AGGTAAAGGC	GACGCCGCC	1450
ATGAAGCAGC	CGTCGCTGCG	AACGTCGCCA	TGTTAATGCG	CCTGCATGGC	1500
CATGAAGATC	TGCAAGCCAA	TGCGCAAACC	GTTCTTGAGG	TACTGCGCAG	1550
TGGTTCCGCT	TACGACAGAG	TCACCGCACT	GGCGGCACGA	GGGTAA	1596

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2703 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GACGACTTAG	TTTGACGGA	ATCAGCATAG	TTAACACTT	CACTGTGGAA	50
AATGAGGAAA	TATTATTTTT	TTTGCCTTC	GTAATTAATG	GTTATAAGGT	100
CGGCCAGAAA	CCTTTCTAAT	GCAAGCGATG	ACGTTTTTTT	ATGTGTCTGA	150
ATTTGCACTG	TGTCACAATT	CCAAATCTTT	ATTAACAAC	CACCTAAAAC	200
GACGCTGATC	CAGCGTGAAT	ACTGGTTCC	CTTATGTTCA	TCAGATTCTAT	250
TTAACCAAGG	GTTTCTCTT	CATTCTGAT	GAAAGTGCCA	TCTAAAAAGA	300
TGATCTTAAT	AAATCTATTA	AGAATGAGAT	GGAGCACACT	GGATATTTA	350
CTTATGAAAC	TGTTTCACTC	CTTACTTAA	TTTATAGAGT	TACCTCCGC	400
TTTTGAAAAA	TACGCAACGG	CCATTTTTG	CACTTAGATA	CAGATTTCT	450
GCGCTGTATT	GCATTGATTT	GATGCTAAC	CTGTTGTTG	CACTAGCTT	500
AAGTGGTTGA	GATCACATT	CCTTGCTCAT	CCCCGCAACT	CCTCCCTGCC	550
TAATCCCCG	CAGGATGAGG	AAGGTCAACA	TCGAGCCTGG	CAAACTAGCG	600
ATAACGTTGT	GTTGAAAATC	TAAGAAAAGT	GGAACCTCCTA	TGTCACAACC	650
TATTTTTAAC	GATAAGCAAT	TTCAGGAAGC	GCTTCACGT	CAGTGGCAGC	700
GTTATGGCTT	AAATTCTGCG	GCTGAAATGA	CTCCTCGCCA	GTGGTGGCTA	750
GCAGTGAGTG	AAGCACTGGC	CGAAATGCTG	CGTGCTCAGC	CATTGCCAA	800
GCCGGTGGCG	AATCAGCGAC	ATGTTAACTA	CATCTCAATG	GAGTTTTGA	850
TTGGTCGCCT	GACGGGCAAC	AACCTGTTGA	ATCTCGGCTG	GTATCAGGAT	900
GTACAGGATT	CGTTGAAGGC	TTATGACATC	AATCTGACGG	ACCTGCTGGA	950
AGAAGAGATC	GACCCGGCGC	TGGGTAACGG	TGGTCTGGGA	CGTCTGGCGG	1000
CGTGCTTCCT	CGACTCAATG	GCAACTGTCG	GTCAGTCTGC	GACGGGTTAC	1050

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GGTCTGA	ACT ATCAATATGG	TTTGTTC	CGC CAGTCTTTG	TCGATGGCAA	1100
ACAGGTTGAA	GCGCCGGATG	ACTGGCATCG	CAGTAAC	TAC CCGTGGTTCC	1150
GCCACAA	CGA CACTGGAT	GTGCAGGTAG	GGATTGGCGG	TAAAGTGACG	1200
AAAGACGGAC	GCTGGGAGCC	GGAGTTACC	ATTACCGGT	AAGCGTGGGA	1250
TCTCCCCGTT	GTCGGCTATC	GTAATGGCGT	GGCGCAGCCG	CTGCGTCTGT	1300
GGCAGGCGAC	GCACGCGCAT	CCGTTGATC	TGACTAAATT	TAACGACGGT	1350
GATTTCTTGC	GTGCCGAACA	GCAGGGCATC	AATGCGGAAA	AACTGACCAA	1400
AGTTCTCTAT	CCAAACGACA	ACCATACTGC	CGGTAAAAAG	CTGCGCCTGA	1450
TGCAGCAATA	CTTCCAGTGT	GCCTGTT	CGG TAGCGGATAT	TTTGCCTCGC	1500
CATCATCTGG	CGGGGCGTGA	ACTGCACGAA	CTGGCGGATT	ACTAAGTTAT	1550
TCAGCTGAAC	GATACCCACC	CAACTATCGC	GATTCCAGAA	CTGCTGCGCG	1600
TGCTGATCGA	TGAGCACCAG	ATGAGCTGGG	ATGACGCTTG	GGCCATTACC	1650
AGCAAAACTT	TCGCTTACAC	CAACCATA	CTGATGCCAG	AAGCGCTGG	1700
ACGCTGGGAT	GTGAAACTGG	TGAAAGGCTT	ACTGCCGCGC	CACATGCAGA	1750
TTATTAACGA	AATTAAT	CGCTTTAAAA	CGCTGGTAGA	GAAAACCTGG	1800
CCGGGCGATG	AAAAAGTGTG	GGCCAAACTG	GGCGTGGTGC	ACGACAAACA	1850
AGTGCATATG	GCGAACCTGT	GTGTGGTTGG	CGGTTTCGCG	GTGAACGGTG	1900
TTGCGGCGCT	GCAC	CTGGTGGTGA	AAGATCTGTT	CCCCGAATAT	1950
CACCAGCTAT	GGCCGAACAA	ATTCCATAAC	GTCACCAACG	GTATTACCCC	2000
ACGTCGCTGG	ATCAAACAGT	GCAACCCGGC	ACTGGCGGCT	CTGTTGGATA	2050
AATCACTGCA	AAAAGAGTGG	GCTAACGATC	TCGATCAGCT	GATCAATCTG	2100
GTTAAATTGG	CTGATGATGC	GAAATTCCGT	CAGCTTTATC	CGGTGATCAA	2150
GCAGGCGAAT	AAAGTCCGTC	TGGCGGAGTT	TGTGAAAGTT	CGTACCGGTA	2200
TTGACATCAA	TCCACAGGCG	ATTTTCGATA	TTCAGATCAA	ACGTTGCAC	2250
GAGTACAAAC	GCCAGCACCT	GAATCTGCTG	CGTATTCTGG	CGTTGTACAA	2300
AGAAAATT	CGT GAAACCCGC	AGGCTGATCG	CGTACCGCGC	GTCTTCCCT	2350
TCGGCGCGAA	AGCGGCACCG	GGCTACTACC	TGGCTAAGAA	TATTATCTTT	2400
GCGATCAACA	AAAGTGGCTGA	CGTGATCAAC	AACGATCCGC	TGGTTGGCGA	2450
TAAGTTGAAG	GTGGTGT	TGCCGGATTA	TTGCGTT	CGCGCGGAAA	2500
AACTGATCCC	GGCGGCGGAT	ATCTCCGAAC	AAATTTGAC	TGCAGGTAAA	2550
GAAGCTTCCG	GTACCGGCAA	TATGAAACTG	GGCGCTCAATG	GTGCGCTTAC	2600
TGTCGGTACG	CTGGATGGGG	CGAACGTTGA	AATCGCCGAG	AAAGTCGGTG	2650
AAGAAAATAT	CTTTATTTT	GGTCATACGG	TCAAACAAGT	GAAGGCAATC	2700
GAC					2703

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(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1391 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AGAGAAGCCT	GTCGGCACCG	TCTGGTTTGC	TTTGCCACT	GCCCCGGTG	50
AAGGCATTAC	CCGGCGGGAT	GCTTCAGCGG	CGACCGTGAT	GCGGTGCGTC	100
GTCAGGCTAC	TGCGTATGCA	TTGCAGACCT	TGTGGCAACA	ATTTCTACAA	150
AACACTTGAT	ACTGTATGAG	CATACAGTAT	AATTGCTTCA	ACAGAACATA	200
TTGACTATCC	GGTATTACCC	GGCATGACAG	GAGTAAAAAT	GGCTATCGAC	250
GAAAACAAAC	AGAAAGCGTT	GGCGGCAGCA	CTGGGCCAGA	TTGAGAAACA	300
ATTTGGTAAA	GGCTCCATCA	TGCGCCTGGG	TGAAGACCGT	TCCATGGATG	350
TGGAAACCAT	CTCTACCGGT	TCGCTTCAC	TGGATATCGC	GCTTGGGCA	400
GGTGGTCTGC	CGATGGGCCG	TATCGTCGAA	ATCTACGGAC	CGGAATCTTC	450
CGGTAAAACC	ACGCTGACGC	TGCAGGTGAT	CGCCGCAGCG	CAGCGTGAAG	500
GTAAAACCTG	TGCGTTTATC	GATGCTGAAC	ACGCGCTGGA	CCCAATCTAC	550
GCACGTAAAC	TGGCGTCGA	TATCGACAAC	CTGCTGTGCT	CCCAGCCGGA	600
CACCGGCGAG	CAGGCACTGG	AAATCTGTGA	CGCCCTGGCG	CGTTCTGGCG	650
CAGTAGACGT	TATCGTCGTT	GACTCCGTGG	CGGCACTGAC	GCCGAAAGCG	700
GAAATCGAAG	GCGAAATCGG	CGACTCTCAC	ATGGGCCTTG	CGGCACGTAT	750
GATGAGCCAG	GCGATGCGTA	AGCTGGCGGG	TAACCTGAAG	CAGTCCAACA	800
CGCTGCTGAT	CTTCATCAAC	CAGATCCGTA	TGAAATTGG	TGTGATGTTTC	850
GGTAACCCCG	AAACCACATAC	CGGTGTTAAC	CGGCTGAAAT	TCTACGCCCTC	900
TGTTCGTCTC	GACATCCGTC	GTATCGGCGC	GGTGAAGAG	GGCGAAAACG	950
TGGTGGGTAG	CGAAACCCGC	GTGAAAGTGG	TGAAGAACAA	AATCGCTGCG	1000
CCGTTAAAC	AGGCTGAATT	CCAGATCCTC	TACGGCGAAG	GTATCAACTT	1050
CTACGGCGAA	CTGGTTGACC	TGGGCGTAAA	AGAGAAGCTG	ATCGAGAAAG	1100
CAGGGCGCTG	GTACAGCTAC	AAAGGTGAGA	AGATCGGTCA	GGGTAAAGCG	1150
AATGCGACTG	CCTGGCTGAA	AGATAACCCG	GAAACCGCGA	AAGAGATCGA	1200
GAAGAAAGTA	CGTGAGTTGC	TGCTGAGCAA	CCCGAACTCA	ACGCCGGATT	1250
TCTCTGTAGA	TGATAGCGAA	GGCGTAGCAG	AAACTAACGA	AGATTTTTAA	1300

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TCGTCTTGT	TGATACACAA	GGTCGCATC	TGCGGCCCTT	TTGCTTTTTT	1350
AAGTTGTAAG	GATATGCCAT	GACAGAATCA	ACATCCCGTC	G	1391

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 238 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TCGCCAGGAA	GGCGGCATTC	GGCTGGTCA	GAGTGACCTG	CAGCGTGGTG	50
TCGTTCAAGCG	CTTCACCC	CAACGTCTCG	GGTCCCTTTT	GCCCGAGGGC	100
AATCTCGCGG	GCGTTGGCGA	TATGCATATT	GCCAGGGTAG	CTCGCGTAGG	150
GGGAGGCTGT	TGCCGGCGAG	ACCAGCCGTT	GCCAGCTCCA	GACGATATCC	200
TGCGCTGTAA	TGGCCGTGCC	GTCAGACCAG	GTCAGACC		238

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 385 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Klebsiella pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CAGCGTAATG	CGCCCGGGCA	TAACGGCGCC	ACTATCGACA	GTCAGTTCGT	50
CAGCCTGCAG	CCTGGGCTGA	ATCTGGGACC	ATGGCGCCTG	CCGAACTACA	100
GCACCTATAG	CCACAGCGAT	AACAAACAGCC	GCTGGGAGTC	GGTTTACTCC	150
TATCTTGGCC	GCGATATTCA	CACCCCTACGC	AGCCAGCTGG	TGGTCGGTAA	200
TACGTATAACC	TCTTCCGGCA	TTTCGACAG	TTTGAGTTTT	ACCGGTCTGC	250
AGCTCAGTTC	GACAAAGAGA	TGCTGCCGGA	TAGCCTGCAT	GCTTTGCGCC	300
GACGATTGCA	GGGATCGCGC	GCACCAACCGC	GGAGGTCTCG	GTTTATCAGA	350

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ATGGTTACAG CATTATATAAA ACCACCGTCG CTACC

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(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CTCTATATT	AGGACGAACA	TATCTGGACC	TCTGGCGGGG	TCAGTTCCGG	50
CTTGATCGC	CCTGCACCCG	CAGCGGGTGA	TCGCCCTCA	TCTGCTACTG	100
CGGCCTGCA	ACAGGCGACG	ATCGATGACG	TTATTCCTGG	CCAGCAAACA	150
GCAGACCAAT	TAAGGTCTGA	TAGTGGCTCT	CTTCCTCCGG	CGCGCGACGG	200
TCCAGGCGGC	TCAACAGTTT	GGTGCATAGC	GCTTTGCGGT	TGAGATGACG	250
CCCTTCGTTA	AGAATATCCA	TCACGATCTC	CGTCCATGGA	GAGTAGCGTT	300
TATTCCAGAA	TAGGGTTTTT	CAGGATCTCA	TGGATCTGCG	CCTGCTTATC	350
GCTATTTGT	AACCAGATCG	CATAAAAGTGG	ACGGGATAAC	GTAGCGCTGT	400
CCATGACCGT	ATGTAACCCA	TGCTTCTCTT	TCGCCAGCG	AGCAGGTAGC	450
CAACAGCAGC	CG				462

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCTGACCGCT	AAACTGGGTT	ACCCGATCAC	TGACGATCTG	GACATCTACA	50
CCCGTCTGGG	CGGCATGGTT	TGGCGCGCTG	ACTCCAAAGG	CAACTACGCT	100
TCAACCGGGG	TTTCCCGTAG	CGAACACGAC	ACTGGCGTTT	CCCCAGTATT	150
TGCTGGCGGC	GTAGAGTGGG	CTGTTACTCG	TGACATCGCT	ACCCGTCTGG	200

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AATACCAGTG	GGTTAACAAAC	ATCGGCGACG	CGGGCACTGT	GGGTACCCGT	250
CCTGATAACG	GCATGCTGAG	CCTGGGCAGTT	TCCTACCGCT	TCGGTCAGGA	300
AGATGCTGCA	CCGGTTGTTG	CTCCGGCTCC	GGCTCCGGCT	CCGGAAGTGG	350
CTACCAAGCA	CTTCACCCCTG	AAGTCTGACG	TTCTGTTCAA	CTTCAACAAA	400
GCTACCCCTGA	AACCGGAAGG	TCAGCAGGCT	CTGGATCAGC	TGTACACTCA	450
GCTGAGCAAC	ATGGATCCGA	AAGACGGTTC	CGCTGTTGTT	CTGGGCTACA	500
CCGACCGCAT	CGGTTCCGAA	GCTTACAACC	AGCAGCTGTC	TGAGAAACGT	550
GCTCAGTCCG	TTGTTGACTA	CCTGGTTGCT	AAAGGCATCC	CGGCTGGCAA	600
AATCTCCGCT	CGCGGCATGG	GTGAATCCAA	CCCGGTTACT	GGCAACACCT	650
GTGACAACGT	GAAAGCTCGC	GCTGCCCTGA	TCGATTGCT	GGCTCCGGAT	700
CGTCGTGTAG	AGATCGAAGT	TAAAGGTATC			730

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CGCTACTGTT	TAAATCTCAT	TTGAAACATC	GCAAAGTCAG	TGAACCACAT	50
ATTCGAGGAT	GGCATGCACT	AGAAAATATT	AATAAGATT	TAGCGAAACC	100
TAATCAGCGC	AATATCGCTT	AATTATTTTA	GGTATGTTCT	CTTCTATCCT	150
ACAGTCACGA	GGCAGTGTG	AACTTGATCC	TCATTTATT	AATCACATGA	200
CCAATGGTAT	AAGCGTCGTC	ACATA			225

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(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ACATTTAAA	TAGGAAGCCA	CCTGATAACA	TCCCCGCAGT	TGGATCATCA	50
GATTTATAGC	GGCATTGGT	ATCCGCTAGA	TAAAAGCAGT	CCAACGATCC	100
CGCCAATTGT	TAGATGAAAT	TGGACTATTTC	TTTTTATTG	CTCCGCTTTA	150
TCACAGTGGT	TTTCGCTTG	CCGCCCCGT	GCGCCAACAG	CTAAGAACAC	200
GCACGCTCTT	TAATGTGTTA	GGCCCATTAA	TTAATCCAGC	GCGTTCCGCC	250
TTTAGCATTA	ATTGGTGTTT	ATAGTCCTGA	ATTATTAATG	CCTATTGCAG	300
ATACCTTAAA	TGTCTGGGC	TACAAACGTG	CGGCAGTGGT	CCATAGTGGT	350
GGAATGGATG	AAGTGTCAATT	ACATGCTCCC	ACACAAGTGG	CTGAGTTACA	400
CA					402

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CTGAAACGCA	TTTATGCGGG	AGTCAGTGAA	ATCATCACTC	AATTTTCACC	50
CGATGTATTT	TCTGTTGAAC	AAGTCTTAT	GGCAAAAAAT	GCAGACTCAG	100
CATTAATT	AGGCCAAGCA	AGAGGTGTGG	CGATTTAGC	GGCAGTCAAT	150
AATGATC					157

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(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1348 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TTTCTCTTTA	AAATCAATT	TTAAAGAAAT	TATTAATAAT	TAAC	TTGATA	50
CTGTATGATT	ATACAGTATA	ATGAGTTCA	ACAAGCAAA	TCAT	ATACGT	100
TTTAATGGTA	GTGACCCATC	TTTATGCTTC	ACTGCCAGA	GGGAGATAAC		150
ATGGCTATTG	ATGAAAACAA	ACAAAAAGCA	TTGGCCGCAG	CACTTGGTCA		200
AATTGAAAAG	CAATTGGTA	AAGGTTCTAT	CATGCGTCTG	GGCGAAGACC		250
GTTCCATGAA	CGTAGAAACT	ATCTCTACAG	GATCTTTATC	ATTAGACGTT		300
GCTTTAGGTG	CAGGTGGATT	GCCACGTGGC	CGTATTGTTG	AAATCTATGG		350
CCCTGAATCT	TCTGGTAAAA	CAACCTTGAC	TCTACAAGTT	ATTGCC	CTCTG	400
CTCAGCGTGA	AGGAAAATT	TGTGCATTTA	TTGATGCTGA	ACATGC	CATTA	450
GACCCAATTT	ATGCTCAAAA	GCTAGGTGTC	GATATCGATA	ATCTACT	CTG	500
CTCTCAACCT	GACACAGGTG	AAACAAGCTCT	GGAAATTGTT	GATGCATTAT		550
CTCGCTCTGG	TGCGGTGCGAT	GTTATTGTCG	TGGACTCCGT	GGCAGC	CATTA	600
ACACCAAAAG	CTGAAATTGA	AGGTGAAATT	GGTGATTTCAC	ACGTTGGTTT		650
AGCCGCACGT	ATGATGAGCC	AAGCTATGCG	TAAACTAGCG	GGTAAC	CTTA	700
AAAACTCTAA	TACACTGCTG	ATTTTCATTA	ACCAAATTG	TATGAAAATC		750
GGTGTATGTT	TTGGTAACCC	AGAAACCACG	ACCGGTGGTA	ATGCGCTTAA		800
ATTCTATGCT	TCTGTTGCGT	TAGACATTG	TCGCATTGGC	TCTGTCAAA		850
ATGGTGTGTA	AGTCATTGGT	AGTGAGACTC	GGCTTAAAGT	TGTTAAAAT		900
AAAGTGGCTG	CACCGTTAA	ACAAGCTGAA	TTCCAAATT	TGTACGGTGA		950
AGGTATTAAT	ACCTATGGCG	AACTGATTGA	TTTAGGTGTT	AAACATAAGT		1000
TAGTAGAGAA	AGCAGGTGCT	TGGTATAGCT	ACAATGGCGA	AAAAATTGGT		1050
CAAGGTAAAG	CTAACCGAAC	CAATTACTTA	AAAGAACATC	CTGAAATGTA		1100
CAATGAGTTA	AACACTAAAT	TGCGTGAAT	GTGTTAAAT	CATGCTGGTG		1150
AATTCAACAAG	TGCTGCGGAT	TTTGCAGGTG	AAGAGTCAGA	CAGTGATGCT		1200
GACGACACAA	AAGAGTAATT	AGCTGGTTGT	CATGCTGTTT	GTGTGAAAAT		1250
AGACCTTAAA	TCATTGGCTA	TTATCACGAC	AGCATCCCAT	AGAATAACTT		1300

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GTTTGTATAA ATTTTATTCA GATGGCAAAG GAAGCCTTAA AAAAGCTT 1348

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2167 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGTACCGCTG	GCCGAGCATC	TGCTCGATCA	CCACCAGCCG	GGCGACGGGA	50
ACTGCACGAT	CTACCTGGCG	AGCCTGGAGC	ACGAGCGGGT	TCGCTTCGTA	100
CGGCGCTGAG	CGACAGTCAC	AGGAGAGGAA	ACGGATGGGA	TCGCACCAGG	150
AGCGGGCGCT	GATCGGCCTG	CTGTTCTCCG	AAACCGGCGT	CACCGCCGAT	200
ATCGAGCGCT	CGCACCGCGTA	TGGCGCATTG	CTCGCGGTGCG	AGCAACTGAA	250
CCCGGAGGGC	GGCGTCGGCG	GTCGCCCGAT	CGAAACGCTG	TCCCAGGACC	300
CCGGCGGCCA	CCCGGACCGC	TATCGGCTGT	GCGCCGAGGA	CTTCATTGCG	350
AACCGGGGGG	TACGGTTCCCT	CGTGGGCTGC	TACATGTCGC	ACACGCGCAA	400
GGCGGTGATG	CCGGTGGTCG	AGCGCGCCGA	CGCGCTGCTC	TGCTACCCGA	450
CCCCCTACGA	GGGCTTCGAG	TATTGCGCCGA	ACATCGTCTA	CGGCGGTCCG	500
GCGCCGAACC	AGAACAGTGC	GCCGCTGGCG	GCGTACCTGA	TTCGCCACTA	550
CGCGGAGCGG	GTGGTGTCA	TCGGCTCGGA	CTACATCTAT	CCGCGGGAAA	600
GCAACCATGT	GATGCGCCAC	CTGTATCGCC	AGCACGGCGG	CACGGTGCTC	650
GAGGAAATCT	ACATTCCGCT	GTATCCCTCC	GACGACGACT	TGCAGCGCGC	700
CGTCGAGCGC	ATCTACCAAGG	CGCGCGCCGA	CGTGGTCTTC	TCCACCGTGG	750
TGGGCACCGG	CACCGCCGAG	CTGTATCGCG	CCATCGCCCG	TCGCTACGGC	800
GACGGCAGGC	GGCCGCCGAT	CGCCAGCCTG	ACCACCAAGCG	AGGCGGAGGT	850
GGCGAAGATG	GAGAGTGACG	TGGCAGAGGG	GCAGGTGGTG	GTCGCGCCTT	900
ACTTCTCCAG	CATCGATACG	CCCGCCAGCC	GGGCCTTCGT	CCAGGCCCTGC	950
CATGGTTCT	TCCCCGGAGAA	CGCGACCATC	ACCGCCTGGG	CCGAGGCGGC	1000
CTACTGGCAG	ACCTTGTTCG	TCGGCCGCGC	CGCGCAGGCC	GCAGGCAACT	1050
GGCGGGTGGA	AGACGTGCAG	CGGCACCTGT	ACGACATCGA	CATCGACGCG	1100
CCACAGGGGC	CGGTCCGGGT	GGAGCGCCAG	AACAACCACA	GCCGCCTGTC	1150
TTCGCGCATC	GCGGAAATCG	ATGCGCGCGG	CGTGGTCCAG	GTCCGCTGGC	1200
AGTCGCCCCA	ACCGATTGCG	CCCGACCCCTT	ATGTCGTCGT	GCATAACCTC	1250

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GACGACTGGT	CCGCCAGCAT	GGGCGGGGGA	CCGCTCCCAT	GAGGCCAAC	1300
TCGCTGCTCG	GCAGCCTGCG	CGAGTTGCAG	GTGCTGGTCC	TCAACCCGCC	1350
GGGGGAGGTC	AGCGACGCC	TGGTCTTGCA	GCTGATCCGC	ATCGGTTGTT	1400
CGGTGCGCCA	GTGCTGGCCG	CCGCCGGAAG	CCTTCGACGT	GCCGGTGGAC	1450
GTGGTCTTCA	CCAGCATTTC	CCAGAATGGC	CACCAACGACG	AGATCGCTGC	1500
GCTGCTCGCC	GCCGGGACTC	CGCGCACTAC	CCTGGTGGCG	CTGGTGGAGT	1550
ACGAAAGCCC	CGCGGTGCTC	TCGCAGATCA	TCGAGCTGGA	GTGCCACGGC	1600
GTGATCACCC	AGCCGCTCGA	TGCCCACCGG	GTGCTGCCGT	TGCTGGTATC	1650
GGCGCGGCGC	ATCAGCGAGG	AAATGGCGAA	GCTGAAGCAG	AAGACCGAGC	1700
AGCTCCAGGA	CCGCATCGCC	GGCCAGGCC	GGATCAACCA	GGCCAAGGTG	1750
TTGCTGATGC	AGGCCATGG	CTGGGACGAG	CGCGAGGCGC	ACCAGCACCT	1800
GTCCGCGGAA	GCGATGAAGC	GGCGCGAGCC	GATCCTGAAG	ATCGCTCAGG	1850
AGTTGCTGGG	AAACGAGCCG	TCCGCCTGAG	CGATCCGGGC	CGACCAGAAC	1900
AATAACAAGA	GGGGTATCGT	CATCATGCTG	GGACTGGTTC	TGCTGTACGT	1950
TGGCGCGGTG	CTGTTCTCA	ATGCCGTCTG	GTTGCTGGGC	AAGATCAGCG	2000
GTCGGGAGGT	GGCGGTGATC	AACTTCCTGG	TCGGCGTGCT	GAGCGCCTGC	2050
GTCGCGTTCT	ACCTGATCTT	TTCCCGAGCA	GCCGGGCAGG	GCTCGCTGAA	2100
GGCCGGAGCG	CTGACCCCTGC	TATTCGCTTT	TACCTATCTG	TGGGTGGCCG	2150
CCAACCAGTT	CCTCGAG				2167

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1872 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GAATTCCCGG	GAGTCCCCGA	CGCAGCCACC	CCCAAAACAC	TGCTAAGGGA	50
GCGCCTCGCA	GGGCTCCTGA	GGAGATAGAC	CATGCCATT	GGCAAGCCAC	100
TGGTGGGCAC	CTTGCTCGCC	TCGCTGACGC	TGCTGGGCCT	GGCCACCGCT	150
CACGCCAAGG	ACGACATGAA	AGCCGCGAG	CAATACCAGG	GTGCCGCTTC	200
CGCCGTCGAT	CCCGCTCACG	TGGTGCGCAC	CAACGGCGCT	CCCGACATGA	250
GTGAAAGCGA	GTTCAACGAG	GCCAAGCAGA	TCTACTTCCA	ACGCTGCGCC	300
GGTTGCCACG	GCGCCTGCG	CAAGGGGCC	ACCGGCAAGC	CGCTGACCCC	350

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GGACATCACCC	CAGCAACGCG	GCCAGCAATA	CCTGGAAGCG	CTGATCACCT	400
ACGGCACCCCC	GCTGGGCATG	CCGAACCTGGG	GCAGCTCCGG	CGAGCTGAGC	450
AAGGAACAGA	TCACCCCTGAT	GGCCAAGTAC	ATCCAGCACA	CCCCGCCGCA	500
ACCGCCGGAG	TGGGGCATGC	CGGAGATGCG	CGAATCGTGG	AAGGTGCTGG	550
TGAAGCCGGA	GGACCGGCCG	AAGAAACAGC	TCAACGACCT	CGACCTGCC	600
AACCTGTTCT	CGGTGACCCCT	GCGCGACGCC	GGGCAGATCG	CCCTGGTCGA	650
CGGCGACAGC	AAAAAGATCG	TCAAGGTCAT	CGATACCGGC	TATGCCGTGC	700
ATATCTCGCG	GATGTCCGCT	TCCGGCCGCT	ACCTGCTGGT	GATCGGCCGC	750
GACGCGCGGA	TCGACATGAT	CGACCTGTGG	GCCAAGGAGC	CGACCAAGGT	800
CGCCGAGATC	AAGATCGGCA	TCGAGGCGCG	CTCGGTGGAA	AGCTCCAAGT	850
TCAAGGGCTA	CGAGGACCGC	TACACCATCG	CCGGCGCCTA	CTGGCCGCCG	900
CAGTCGCGA	TCATGGACGG	CGAGACCCCTG	GAACCGAAGC	AGATCGTCTC	950
CACCCGGCGC	ATGACCGTAG	ACACCCAGAC	CTACCACCCG	GAACCGCGCG	1000
TGGCGGCGAT	CATCGCCTCC	CACGAGCACC	CCGAGTTCAT	CGTCAACGTG	1050
AAGGAGACCG	GCAAGGT CCT	GCTGGTCAAC	TACAAGGATA	TCGACAACCT	1100
CACCGTCACC	AGCATCGGTG	CGGCGCCGTT	CCTCCACGAC	GGCGGCTGGG	1150
ACAGCAGCCA	CCGCTACTTC	ATGACCGCCG	CCAACAACTC	CAACAAGGTT	1200
GCCGTGATCG	ACTCCAAGGA	CCGTCGCTG	TCGGCCCTGG	TCGACGTCGG	1250
CAAGACCCCG	CACCCGGGGC	GTGGCGCCAA	CTTCGTGCAT	CCCAAGTACG	1300
GCCCCGTGTG	GAGCACCAGC	CACCTGGCG	ACGGCAGCCT	CTCGCTGATC	1350
GGCACCGATC	CGAAGAACCA	TCCGCAGTAC	GCCTGGAAGA	AAGTCGCCGA	1400
ACTACAGGGC	CAGGGCGGCG	GCTCGCTGTT	CATCAAGACC	CATCCGAAGT	1450
CCTCGCACCT	CTACGTCGAC	ACCACCTTCA	ACCCCGACGC	CAGGATCAGC	1500
CAGAGCGTCG	CGGTGTTCGA	CCTGAAGAAC	CTCGACGCCA	AGTACCAAGT	1550
GCTGCCGATC	GCCGAATGGG	CCGATCTCGG	CGAAGGCGCC	AAGCGGGTGG	1600
TGCAGCCCCA	GTACAACAAG	CGCGGCGATG	AAGTCTGGTT	CTCGGTGTGG	1650
AACGGCAAGA	ACGACAGCTC	CGCGCTGGTG	GTGGTGGACG	ACAAGACCC	1700
GAAGCTCAAG	GCCGTGGTCA	AGGACCCCG	GCTGATCACC	CCGACCGGTA	1750
AGTTCAACGT	CTACAAACACC	CAGCACGACG	TGTACTGAGA	CCCGCGTGC	1800
GGGCACGCC	CGCACGCTCC	CCCCTACGAG	GAACCGTGAT	GAAACCGTAC	1850
GCACGTCTT	CGCTGCTCGC	CA			1872

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(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3451 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TCGAGACGGG	AAGCCACTCT	CTACGAGAAG	ACAGAAGCCC	CTCACAGAGG	50
CCTCTGTCTA	CGCCTACTAA	AGCTCGGCTT	ATTCAATATGT	ATTTATATTC	100
TTTCAATAGA	TCACTCAGCG	CTATTTAAG	TTCACCCCTCT	GTAAGTTCAC	150
CTGGGCGCTC	TTTCTTCCT	TCGGTAAAGC	TGTCGGCCAG	ACCAAACATT	200
AAACTCAAGC	ATCTCCAAG	CGATGCATCA	TCTTGGGCCA	GCATCCCTGA	250
ATCGCGCGTC	GGACCTCCAA	GTCTTAAAAA	ATTCTTCGCT	GAAGGTTTTC	300
CCATCAATCG	ATGAGGCTAA	TAGCTCTTT	GCAATATCTA	TCATTTCCAT	350
GCTCACCTTA	AAGCACCTCA	TTTTTCATGT	AAAAATTGTA	TTGATCCGTG	400
CCAGACTCAA	TCCTCCACCC	AGAAACAAAC	ATCCCACCTC	CTCCAATGAT	450
AACAACAATA	TTAGTCCTGG	CATTGTAATG	TACTTTGAG	TTTACTTCGG	500
AGTGGTAAGT	CCCTTTTCT	ACGGTTGCAG	GATCAGCAAG	GTGCTCAAGA	550
ATTTTATCCC	TAAACTCTGC	AAGCGTTCCA	TTGTTGGCGC	TTTTTCACC	600
CAGCCCAAAA	TCATATTTGT	GGCTATCAA	TTTTTCTGT	AGTTGCCTCC	650
GTGTGAAGAT	ACCACTATCA	AGAGGACTAC	TGAGCATTAC	ATAAACAGGT	700
TTGACTCCAG	AATCCGCCGG	GAAAATCACG	ATCAGATCGT	TTAGGTCCAG	750
TACCATTCAC	GGATAGGACT	CCGGGCCGGT	CTTCAACGGT	GTGAGGGCCG	800
CTCCCTCATA	TACCGGCACC	GGCTTCGGTA	TGACCGGAGT	GGTACTCGAA	850
GGGTCTGGT	TTCTGGAGG	ACTCGCCGGC	GTCCAAGTCA	GGATCAGTGG	900
CGCGCTTCT	GCGACCGTAG	AGGGAACCGT	AACCTCGTAC	AGTCCTGTTG	950
CGCGTATA	GGCCCCATCC	GGACCGGAAC	GCTTTGGAA	CGCTCACACC	1000
ATCGGTCTGA	CCACCGAAAG	GTCGTCGTGT	TGCCTCGCCG	CTCGTTGGTC	1050
AGGCGCATCG	GCAGATCGAC	GGTACCGCTG	GCTTTTGCAA	CCGCGTTCAG	1100
GTTACGCTT	GGGGGAAGCC	CCAATTAGC	GGCATCCATG	CCCAGGGCGT	1150
AACGAACGCT	ATCGGGCGTT	TGGTCCGCC	ATTGCTCGGC	AGTCCGGGAG	1200
AGTAGGTCAAGC	ACTGGCAAGC	CACGGCCATC	ACCGAGGTGC	TGAAGCCAGG	1250
ACCGCCAGGA	CGGCAATCGC	ATCGGAGATC	GCTTGAGCAA	GGGATGCGGC	1300

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GCCTGTGCGA	CCTGGATCAG	ACCCCGCTGC	GGCGGTGGCG	CACCCGCTGC	1350
CATTGGCTGG	CATGGCATAA	GTATTGGCAG	CCCTGATCGC	CGCTTGACGA	1400
GCGATTTCTCCT	TGCGCCTTGC	CGTTTCGGCG	TTCAGCTTGT	CCAGCCGTGC	1450
TTGCAGGCTG	GCGATTTCAT	CCACTAGGTA	GGACATCGGC	GTTGTAGGTT	1500
GCCTTTGTT	TCTCCAGTGC	ATTGGGTGCC	TTGGCAATCA	AGGCATTGTT	1550
TGCAGTCTGC	AATTCTTCTT	ATTGCGATCG	CCTGCGTAAG	GAGTTGAGTA	1600
GCGCGTTCAA	GCCACTGCTC	TGGCGTTGGA	TTGGTCAGTT	GAGGCAAAGC	1650
ATTCCCAGCC	TGGTCAAGCT	CGGACTGCAC	TTTTTCTCG	ACATTGCCT	1700
TCCTGGCCTT	GTAGTCCGCC	TCCACCTCAG	CAGCGGCTCG	CTGGGCTTCT	1750
GCTTCCAATG	ACCGGGCTTT	ATTCTCCAGC	TCTTGAGACG	TTTGTTCAA	1800
GATAGCGATT	TGCGCCTTAT	AGATATCGGC	GCTGTACGCT	TTGGCCAGCT	1850
CACTCATATG	GCGATCCAGG	AACTCTCCAT	AGAATTTCG	GCTGGCCAGC	1900
AACTGACTCT	GGTACATCGA	CTCTGACTTC	TGAGGAAAGT	CTGAAGCCGT	1950
ATAAAAGATTG	GCCGGGCGAT	CCTCAATGAC	CTTTAGCGAT	TTTGCTTTGG	2000
CATCCATGAG	TGCATCAACG	ATACTCTTT	CATCGCGGAT	GTCATTGGCA	2050
CTGACCGCTT	TACCTGGCAA	CCCCGTTCA	CTCTTGAGTT	CATCAACCTC	2100
CTTCAGGGTT	TCATTTTCA	GGTTTTCTT	GAGTTCTGAA	TGGGACTTAT	2150
CAAGCGTACT	TCTTAGCTTC	CTGTACTCCT	GCATTCCAGT	ACCGACATAC	2200
GGACTTGGTC	CTGGTGGGAC	AAATGGTGA	GTACCGTAGC	TTGATCGAGC	2250
AGGAATATAC	TGGATTATGT	CACGCCAAC	ACCCTGCACA	TGTGTAATAA	2300
CCATCGAACCC	AGGTTCGTAA	TCATTGACAG	CCATAGATCG	CCCCTACATT	2350
AATTTGAAAG	TGTAATGTAT	TGAGCGACTC	CCACCTAGAG	AACCCTCTCC	2400
CAGTCATAAA	GCCCCAATGC	ATCGGCAATA	CACTGCAATC	AACTTCAATA	2450
TCCCGTGT	AGATGATCCA	GAAGGTGGC	TCTCTGCCT	CTTATAATCG	2500
CGCCTGCGTC	AAACGGTCAT	TTCCCTAACG	CACACCTCAT	CTACCCGGC	2550
CAGTCACGGA	AGCCGCATAC	CTTCGGTTCA	TTAACGAACT	CCCACTTTCA	2600
AAATTCCATCC	ATGCCGCCCC	TTCGCGAGCT	TCCGGACAAA	GCCACGCTGA	2650
TTGCGAGCCC	AGCGTTTTG	ATTGCAAGCC	GCTGCAGCTG	GTCAGGCCGT	2700
TTCCGCAACG	CTTGAAGTCC	TGGCCGATAT	ACCGGCAGGG	CCAGCCATCG	2750
TTCGACGAAT	AAAGCCACCT	CAGCCATGAT	GCCCTTTCCA	TCCCCAGCGG	2800
AAACCCCGACA	TGGACGCCAA	AGCCCTGCTC	CTCGGCAGCC	TCTGCCCTGGC	2850
CGCCCCATTC	GCCGACGCCG	CGACGCTCGA	CAATGCTCTC	TCCGCCCTGCC	2900
TCGCCGCCCG	GCTCGGTGCA	CCGCACACGG	CGGAGGGCCA	GTTGCACCTG	2950
CCACTCACCC	TTGAGGCCCG	GCGCTCCACC	GGCGAATGCG	GCTGTACCTC	3000
GGCGCTGGTG	CGATATCGGC	TGCTGGCCAG	GGGCGCCAGC	GCCGACAGCC	3050
TCGTGCTTCA	AGAGGGCTGC	TCGATAGTCG	CCAGGACACG	CCGCGCACGC	3100
TGACCCCTGGC	GGCGGACGCC	GGCTTGGCGA	GGGGCCCGA	ACTGGTCGTC	3150

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ACCCCTGGGTT	GTCAGGCGCC	TGACTGACAG	GCCGGGCTGC	CACCACCAAGG	3200
CCGAGATGGA	CGCCCTGCAT	GTATCCTCCG	ATCGGCAAGC	CTCCCGTTCG	3250
CACATTCAACC	ACTCTGCAAT	CCAGTTCATATA	AATCCCATAA	AAGCCCTCTT	3300
CCGCTCCCCG	CCAGCCTCCC	CGCATCCCGC	ACCCTAGACG	CCCCGCCGCT	3350
CTCCGCCGGC	TCGCCCCACA	AGAAAAAACCA	ACCGCTCGAT	CAGCCTCATC	3400
CTTCACCCAT	CACAGGAGCC	ATCGCGATGC	ACCTGATACC	CCATTGGATC	3450
C					3451

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGGTTCAGCA	AGCGTTCAAGG	GGCGGTTCAAG	TACCCCTGTCC	GTACTCTGCA	50
AGCCGTGAAC	GACACGACTC	TCGCAGAACG	GAGAAACACC	ATGAAAGCAC	100
TCAAGACTCT	CTTCATCGCC	ACCGCCCTGC	TGGGTTCCGC	CGCCGGCGTC	150
CAGGCCGCCG	ACAACCTCGT	CGGCCTGACC	TGGGGCGAGA	CCAGCAACAA	200
CATCCAGAAA	TCCAAGTCGC	TGAACCGCAA	CCTGAACAGC	CCGAACCTCG	250
ACAAGGTGAT	CGACAAACACC	GGCACCTGGG	GCATCCGCGC	CGGCCAGCAG	300
TTCGAGCAGG	GCCGCTACTA	CGCGACCTAC	GAGAACATCT	CCGACACCAAG	350
CAGCGGCAAC	AAGCTGCCGC	AGCAGAACCT	GCTCGGCAGC	TACGACGCCCT	400
TCCTGCCGAT	CGGCGACAAC	AACACCAAGC	TGTTCCGGCG	TGCCACCCCTC	450
GGCCTGGTCA	AGCTGGAACA	GGACGGCAAG	GGCTTCAAGC	GCGACAGCGA	500
TGTCGGCTAC	GCTGCCGGC	TGCAGGCCGG	TATCCTGCAG	GAGCTGAGCA	550
AGAATGCCTC	GATCGAAGGC	GGCTATCGTT	ACCTGCGCAC	CAACGCCAGC	600
ACCGAGATGA	CCCCGCATGG	CGGCAACAAAG	CTGGGCTCCC	TGGACCTGCA	650
CAGCAGCTCG	CAATTCTACC	TGGGCGCCAA	CTACAAAGTTC	TAAATGACCG	700
CGCAGCGCCC	GCGAGGGCAT	GCTTCGATGG	CCGGGCCGGA	AGGT	744

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(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2760 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CTGCAGCTGG	TCAGGCCGTT	TCCGCAACGC	TTGAAGTCCT	GGCCGATATA	50
CCGGCAGGGC	CAGCCATCGT	TCGACGAATA	AAGCCACCTC	AGCCATGATG	100
CCCTTTCAT	CCCCAGCGGA	ACCCCGACAT	GGACGCCAAA	GCCCTGCTCC	150
TCGGCAGCCT	CTGCCTGGCC	GCCCCATTCTG	CCGACGCGGC	GACGCTCGAC	200
AATGCTCTCT	CCGCCTGCCT	CGCCGCCCCG	CTCGGTGCAC	CGCACACGGC	250
GGAGGGCCAG	TTGCACCTGC	CACTCACCCCT	TGAGGCCCCG	CGCTCCACCG	300
GCGAATGCGG	CTGTACCTCG	GCGCTGGTGC	GATATCGGCT	GCTGGCCAGG	350
GGCGCCAGCG	CCGACAGCCT	CGTGCTTCAA	GAGGGCTGCT	CGATAGTCGC	400
CAGGACACGC	CGCGCACGCT	GACCCCTGGCG	GCGGACGCCG	GCTTGGCGAG	450
CGGCCGCGAA	CTGGTCGTCA	CCCTGGGTG	TCAGGCGCCT	GACTGACAGG	500
CCGGGCTGCC	ACCACCAGGC	CGAGATGGAC	GCCCTGCATG	TATCCTCCGA	550
TCGGCAAGCC	TCCCCTTCGC	ACATTCAACCA	CTCTGCAATC	CAGTTCATAA	600
ATCCCATAAA	AGCCCTCTTC	CGCTCCCCGC	CAGCCTCCCC	GCATCCCGCA	650
CCCTAGACGC	CCCGCCGCTC	TCCGCCGGCT	CGCCCGACAA	GAAAAACCAA	700
CCGCTCGATC	AGCCTCATCC	TTCACCCATC	ACAGGAGCCA	TCGCGATGCA	750
CCTGATAACCC	CATTGGATCC	CCCTGGTCGC	CAGCCTCGGC	CTGCTCGCCG	800
GCGGCTCGTC	CGCGTCCGCC	GCCGAGGAAG	CCTTCGACCT	CTGGAACGAA	850
TGGGCCAAAG	CCTGCGTGCT	CGACCTCAAG	GACGGCGTGC	GTTCCAGCCG	900
CATGAGCGTC	GACCCGGCCA	TCGCCGACAC	CAACGGCCAG	GGCGTGCTGC	950
ACTACTCCAT	GGTCCCTGGAG	GGCGGCAACG	ACCGCCTCAA	GCTGGCCATC	1000
GACAACGCC	TCAGCATCAC	CAGCGACGGC	CTGACCATCC	GCCTCGAAGG	1050
CGGCGTCGAG	CCGAACAAGC	CGGTGCGCTA	CAGCTACACCG	CGCCAGGCCG	1100
GCGGCAGTTG	GTCGCTGAAC	TGGCTGGTAC	CGATCGGCCA	CGAGAAGCCC	1150
TCGAACATCA	AGGTGTTCAT	CCACGAACGT	AACGCCGGCA	ACCAGCTCAG	1200
CCACATGTCTG	CCGATCTACA	CCATCGAGAT	GGGCGACGAG	TTGCTGGCGA	1250
AGCTGGCGCG	CGATGCCACC	TTCTTCGTCA	GGGCGCACGA	GAGCAACGAG	1300

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ATGCAGCCGA	CGCTCGCCAT	CAGCCATGCC	GGGGTCAGCG	TGGTCATGGC	1350
CCAGACCCAG	CCGCGCCGGG	AAAAGCGCTG	GAGCGAATGG	GCCAGCGGCA	1400
AGGTGTTGTG	CCTGCTCGAC	CCGCTGGACG	GGGTCTACAA	CTACCTCGCC	1450
CAGCAACGCT	GCAACCTCGA	CGATAACCTGG	GAAGGCAAGA	TCTACCGGGT	1500
GCTCGCCGGC	AACCCGGCGA	AGCATGACCT	GGACATCAAA	CCCACGGTCA	1550
TCAGTCATCG	CCTGCACTTT	CCCGAGGGCG	GCAGCCTGGC	CGCGCTGACC	1600
GCGCACCAAGG	CTTGCCACCT	GCCGCTGGAG	ACTTTCACCC	GTCATCGCCA	1650
GCCGCGCGGC	TGGGAACAAC	TGGAGCAGTG	CGGCTATCCG	GTGCAGCGGC	1700
TGGTCGCCCT	CTACCTGGCG	GCGCGCTGT	CGTGGAACCA	GGTCGACCAAG	1750
GTGATCCGCA	ACGCCCTGGC	CAGCCCCGGC	AGCGGCGGGCG	ACCTGGGCGA	1800
AGCGATCCGC	GAGCAGCCGG	AGCAGGCCCAG	TCTGGCCCTG	ACCCCTGGCCG	1850
CCGCGAGAG	CGAGCGCTTC	GTCCGGCAGG	GCACCGGCAA	CGACGAGGCC	1900
GGCGCGGCCA	ACGCGGACGT	GGTGAGCCTG	ACCTGCCCCGG	TCGCGCGCCGG	1950
TGAATGCGCG	GGCCCCGGCGG	ACAGCGGCGA	CGCCCTGCTG	GAGCGCAACT	2000
ATCCCACCTGG	CGCGGAGTTC	CTCGGCGACG	GC GGCGACGT	CAGCTTCAGC	2050
ACCCCGGGCA	CGCAGAACTG	GACGGTGGAG	CGGCTGCTCC	AGGCGCACCG	2100
CCAACTGGAG	GAGCGCGGCT	ATGTGTTCGT	CGGCTACCCAC	GGCACCTTCC	2150
TCGAAGCGGC	GCAAAGCATC	GTCTTCGGCG	GGGTGCGCGC	GCGCAGCCAG	2200
GACCTCGACG	CGATCTGGCG	CGGTTTCTAT	ATCGCCGGCG	ATCCGGCGCT	2250
GGCCTACGGC	TACGCCAGG	ACCAGGAACC	CGACGCACGC	GGCCGGATCC	2300
GCAACGGTGC	CCTGCTGGCG	GTCTATGTGC	CGCGCTCGAG	CCTGCCGGGC	2350
TTCTACCGCA	CCAGCCTGAC	CCTGGCCGGC	CCGGGAGGCGG	CGGGCGAGGT	2400
CGAACGGCTG	ATCGGCCATC	CGCTGCCGCT	GC GGCTGGAC	GCCATCACCG	2450
GCCCCGAGGA	GGAAGGGCGGG	CGCCTGGAGA	CCATTCTCGG	CTGGCCGCTG	2500
GCCGAGCGCA	CCGTGGTGAT	TCCCTCGGCG	ATCCCCACCG	ACCCGCGCAA	2550
CGTGGCGGC	GACCTCGACC	CGTCCAGCAT	CCCCGACAAG	GAACAGGCCA	2600
TCAGCGCCCT	GCCGGACTAC	GCCAGCCAGC	CCGGCAAACC	GCCGCGCGAG	2650
GACCTGAAGT	AACTGCCGCG	ACCGGCCGGC	TCCCTTCGCA	GGAGCCGGCC	2700
TTCTCGGGGC	CTGGCCATAC	ATCAGGTTTT	CCTGATGCCA	GCCCAATCGA	2750
ATATGAATT					2760

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(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 172 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TTGATGAAAT	GCATCGATT	ATAAATTTTC	ATGTACGATT	AAAACGTTTT	50
TACCCCTTACC	TTTTCGTACT	ACCTCTGCCT	GAAGTTGACC	ACCTTTAAAG	100
TGATTCTGTTG	AAATCCATTA	TGCTCATTAT	TAATACGATC	TATAAAAACA	150
AATGGAATGT	GATGATCGAT	GA			172

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GTTCCATTGA	CTCTGTATCA	CCTGTTGAA	CGAACATCCA	TATGTCCTGA	50
AACTCCAACC	ACAGGTTTGA	CCACTTCAA	TTTCAGACCA	CCAAGTTGA	100
CACGTGAAGA	TTCATCTTCT	AATATTCGG	AATTAATATC	ATATTATTAA	150
AATAG					155

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ACATAGAAAA	ACTAAAAGA	TTTACTTTT	TCAAATGGAA	AATAAGGGTA	50
CACACGATAT	TTCCCGTCAT	CTTCAGTTAC	CGGTACAACA	TCCTCTTTAT	100
TAACCTGCAC	ATAATCTGAC	TCCGCTTCAC	TCATCAAAC	ACTAA	145

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TTTCACTGGA	ATTACATTTG	GTCATTACG	TACAGTGACA	ATCGCGTCAG	50
ATAGTTTCTT	CTGGTTAGCT	TGACTCTTAA	CAATCTTGT	TAAATTTGT	100
TTAATTCTTT	GATTCGTA	AGAAATTTA	CTTCTAATT	CTTGTAAATT	150
ATAACTTGCA	TTATCATATA	AATCATAAGT	ATCACATTTT	TGATGAATAC	200
TTTGATATAA	ATCTGACAAT	ACAGGCAGTT	GCTCCATTCT	ATCGTTAAGA	250
ATAGGGTAAT	TAATAG				266

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 845 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

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TGTTAAATTT	CTTTAACAGG	GATTTGTTA	TTTAAATTAA	ACCTATTATT	50
TTGTCGCTTC	TTTCACTGCA	TCTACTGCTT	GAGTTGCTTT	TTCTGAAACC	100
GCCTCTTCA	TTTCACTTGC	TTTTCTGAT	GCTGCTTCTT	TCATTCGCC	150
TACTTTTCT	GACGCTGCTT	CTGTTGCTGA	TTTAATTACT	TCTTCGCAT	200
CTTCCACTTT	CTCTGCTACT	TTATTTTCA	CGTCTGTAGA	AAGCTGCTGT	250
GCTTTTCCT	TTACTTCAGT	CATTGTATTA	GCTGCAGCAT	CTTTGTTTC	300
TGATGCGACT	GATGCTACAG	TTTGCTTCGT	ATCCTCAACT	TTTTGTTTG	350
CTTCTGCTT	ATCAAAACAA	CCTGTCACCGA	CTAAAGCTGA	ACCTAAAACC	400
AATGCTAATG	TTAATTTTT	CATTATTTTC	TCCATAGAAT	AATTTGATTG	450
TTACAAAGCC	CTATTACTTT	GATGCAGTTT	AGTTTACGGG	AATTTTCATA	500
AAAAAGAAAAAA	CAGTAATAGT	AAAACTTAC	CTTCTTTAA	AAAGATTACT	550
TTATAAAAAAA	ACATCTAAGA	TATTGATTTC	TAATAGATTA	TAAAAAAACCA	600
ATAAAAATTTATTTTTGT	AAAAAAAAG	AATAGTTTAT	TTTAAATAAA	650	
TTACAGGAGA	TGCTTGATGC	ATCAATATT	CTGATTATT	ACCATCCCAT	700
AATAATTGAG	CAATAGTTGC	AGGATAAAAT	GATATTGGAT	TTCGTTTCC	750
ATACAGTTCA	GCAACAATT	CTCCCCTAA	GGGCAAATGG	GAAACAATTA	800
ATACAGATT	AACGCCCTCG	TCTTTAGCA	CTTCTAAATA	ATCAA	845

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1598 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GAATAGAGTT	GCACCAATA	GATTGGGCT	TTATAATTGC	CCAGATTTT	50
ATTTATAACA	AAGGGTCCA	AATGAAAAAA	TTTAATCAAT	CTCTATTAGC	100
AACTGCAATG	TTGTTGGCTG	CAGGTGGTGC	AAATGCGGCA	GCGTTTCAAT	150
TGGCGGAAGT	TTCTACTTCA	GGTCTTGGTC	GTGCCTATGC	GGGTGAAGCG	200
GCGATTGCAG	ATAATGCTTC	TGTCGTGGCA	ACTAACCCAG	CTTGATGAG	250
TTTATTTAAA	ACGGCACAGT	TTTCCACAGG	TGGCGTTTAT	ATTGATTCTA	300
GAATTAATAT	GAATGGTGT	GTAACTTCTT	ATGCTCAGAT	AATAACAAAT	350
CAGATTGGAA	TGAAAGCAAT	AAAGGACGGC	TCAGCTTCAC	AGCGTAATGT	400
TGTTCCCGGT	GCTTTGTGC	CAAATCTTA	TTTCGTTGCG	CCAGTGAATG	450

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ATAAATTTCGC	GCTGGGTGCT	GGAATGAATG	TCAATTCGG	TCTAAAAAGT	500
GAATATGACG	ATAGTTATGA	TGCTGGTGT	TTTGGTGGAA	AAACTGACTT	550
GAGTGCTATC	AACTTAAATT	TAAGTGGTGC	TTATCGAGTA	ACAGAAGGTT	600
TGAGCCTAGG	TTTAGGGGT	AATGCGGTTT	ATGCTAAAGC	CCAAGTTGAA	650
CGGAATGCTG	GTCTTATTGC	GGATAGTGT	AAGGATAACC	AAATAACAAG	700
CGCACTCTCA	ACACAGCAAG	AACCATTCA	AGATCTTAAG	AAGTATTG	750
CCTCTAAGGA	CAAATCTGTT	GTGTCATTAC	AAGATAGAGC	CGCTTGGGGC	800
TTTGGCTGGA	ATGCAGGTGT	AATGTATCAA	TTTAATGAAG	CTAACAGAAAT	850
TGGTTTAGCC	TATCATTCTA	AAGTGGACAT	TGATTTGCT	GACCGCACTG	900
CTACTAGTTT	AGAAGCAAAT	GTCATCAAAG	AAGGTTAAAAA	AGGTAATTAA	950
ACCTTTACAT	TGCCAGATTA	CTTAGAACTT	TCTGGTTCC	ATCAATTAAAC	1000
TGACAAACTT	GCAGTGCATT	ATAGTTATAA	ATATACCCAT	TGGAGTCGTT	1050
TAACAAAATT	ACATGCCAGC	TTCGAAGATG	GTAAAAAAGC	TTTGATAAA	1100
GAATTACAAT	ACAGTAATAA	CTCTCGTGT	GCATTAGGGG	CAAGTTATAA	1150
TCTTTATGAA	AAATTGACCT	TACGTGCGGG	TATTGCTTAC	GATCAAGCGG	1200
CATCTCGTCA	TCACCGTAGT	GCTGCAATT	CAGATACCGA	TCGCACTTGG	1250
TATAGTTTAG	GTGCAACCTA	TAAATTACG	CCGAATTAT	CTGTTGATCT	1300
TGGCTATGCT	TACTTAAAG	GCAAAAAAGT	TCACTTAAA	GAAGTAAAAA	1350
CAATAGGTGA	CAAACGTACA	TTGACATTGA	ATACAAC	AAATTATACT	1400
TCTCAAGCAC	ACGCAAATCT	TTACGGTTG	AATTTAAATT	ATAGTTCTA	1450
ATCCGTTAAA	AAATTAGCA	TAATAAAGCA	CAATTCCACA	CTAAGTGTGC	1500
TTTTCTTTA	AAAAACAAAG	CGAAAAATGA	CCGCACTTTA	TTACACTTAT	1550
TACCCCTCGC	CAGTCGGACG	GCTTTGATT	TTATCTGACG	GCGAAACA	1598

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9100 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GTCAAAAAATT	GCGTGCATTC	TAGCGAAAAA	ATGGGCTTTT	GGGAACTGTG	50
GGATTATTAT	AAAATCTTAG	AAAATCTTAC	CGCACTTTA	AGCTATAAAAG	100
TGCGGTGAAA	TTTAGTGGCG	TTTATAATGG	AGAATTACTC	TGGTGTAAATC	150

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CATTCGACTG	TCCAGCTTCC	AGTACCTTCT	GGAACTAATG	TTTTTGTGAG	200
ATAAGGCAAA	ATTTCTTCA	TTTGGGTTTC	TAATGTCCAA	GGTGGATTAA	250
TTACCACCAT	ACCGCTCGCA	GTCATTCTC	GTTGATCGCT	ATCTGGCGA	300
ACGGCGAGTT	CAATTTTAG	AATTTTCTA	ATTCCCCTTG	CTTCTAAACC	350
CTTAAAATA	CGTTTAGTTT	GTTGGCGTAA	TACAAACAGGA	TACCAAATCG	400
CATAAGTGCC	AGTGGCAAA	CGTTTATAGC	CCTCTTCAAT	GGCTTTAACAA	450
ACGAGATCAT	AATCATCTT	TAATTCAAA	GGCGGATCGA	TGAGTACTAA	500
GCCTCGGCGT	TCTTTGGCG	GAAGCGTTGC	TTTGACTTGT	TGAAAGCCAT	550
TGTCACATTT	TACGGTGACA	TTTTTGTGCGT	CGCTAAAATT	ATTGCGAAGA	600
ATTGGATAAT	CGCTAGGATG	AAGCTCGGTC	AATAGTGCAC	GATCTTGTGA	650
GCGCAACAAT	TCCGCGGCAA	TTAATGGAGA	ACCCGGTAA	TAACGTAGTT	700
CTTTGCCACC	ATAATTGAGT	TTTTTGATCA	TTTTTACATA	ACGAGCAATA	750
TCTTCGGGTA	AATCTGTTG	ATCCCACAGG	CGTCCAATAC	CTTCTTTATA	800
TTCCCCCGTT	TTTTCTGATT	CATTGAGGA	TAAACGATAA	CGCCCCACAC	850
CAGAGTGCCT	ATCCAAATAA	AAAAAGCCTT	TTTCTTGAG	TTTAAGATTT	900
TCCAAATGA	GCATTAAC	AATATGTTTC	AAGACATCGG	CATGATTGCC	950
AGCGTGAAAT	GAGTGATGAT	AACTCAGCAT	AATATATTCC	TTATATATTTC	1000
CTTATTGTT	TAATAACGAA	GGCGAGCCAA	TTGACTCGCC	CGATTACACA	1050
CTAAAGTGC	GTCATTTTA	GAAGAGTTCT	TGTGGTTGCG	TCGCTGGCGT	1100
ATTGCCTTCA	TTATTTAACG	GTTGCTGAA	CTCAGTAGGA	ACATAATAAC	1150
CACGCTCTTG	CATTTCCGAA	AGATAGGTAC	GTGTGGTTTC	TGTTCCCGCA	1200
ATAAAATATT	CTTTGCGCCC	ACCGTTGGA	GAAAGCAAAC	CTGTCAAAGT	1250
ATCAATGTTT	TTTTCCACAA	TTTTTGGCGG	TAGCGACAAT	TTACGTTCTG	1300
GCTTATCACT	CAAAGCCGTT	TTCATATAAG	TGATCCAAGC	AGGCATTGCT	1350
GTCCCCGCTC	CTGCTTCTCC	ACGCCAAGT	ACTCGTTGT	TATCATCAAA	1400
CCCGACATAA	GTTGTGGTTA	CTAAGTTGC	ACCAAATCCC	GCATACCAAG	1450
CCACTTTGA	ACTGTTGGTA	GTACCTGTTT	TACCGCCTAT	ATCGCTACGT	1500
TTAATGCTTT	GTGCAATACG	CCAGCTGGTG	CCTTTCCAGT	CTAAACCTTG	1550
TTGCCATAA	ATTGCCGTAT	TTAAGGCACT	ACGAATGAGA	AAAGCAAGTT	1600
CGCCACTAAT	GACACGTGGC	GCATATTCTA	TTTTCGACGA	AGCATTTTTT	1650
GCAGCAGCCA	TTAAATCAAT	CGCATCTTCT	TTAAGTGCAGG	TCATATTGAA	1700
TTGTAATTCT	GGCAGTTCA	GCACAGTTTC	AGGTTGTTGA	TCTAATTCTT	1750
CGCCATTGGT	GCTGTCATCT	GTTGGTTTTA	AGGCATTCTC	GCCTAAAGGA	1800
ATATTGGCAA	AGCCGTTGAT	TTTGTCTTTG	GTTTCGCCAT	AAATTACAGG	1850
TATATCATT	CATTCAATGC	AAGCAATTTC	AGGGTTTGCA	ATAAAATAAGT	1900
CTTTACCCGT	GTTATCTTGA	ATTTTTCAA	TGATATAAGG	TTCAATGAGG	1950
AAGCCACCAT	TATCAAACAC	CGCATAAGCT	CGCGCCATT	CTAATGGTGT	2000

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GAAAGAGGCT	GCGCCAAGTG	CTAAGGCTTC	ACTGGCAAAA	TATTGATCAC	2050
GTTTAAAACC	AAAACGTTGT	AAAAATTCTG	CTGTGAAATC	AATACCTGCC	2100
GTTGGATAG	CACGAATAGC	AATTATATTT	TTGGATTGAC	CTAATCCTAC	2150
GCGTAAACGC	ATCGGGCCAT	CATAACGATC	AGGCGAGTTT	TTCGGTTGCC	2200
ACATTTTTTG	TCCC GGTTTT	TGAATAGAAA	TCGGGCTGTC	TTGTAATACG	2250
CTTGAAGATG	TTAACGCCTT	TTCTAATGCT	GCCCGTAAA	AAAATGGTTT	2300
GATAGAAGAA	CCCACTTGAA	CTAAAGACTG	TGTGGCTCGA	TTGAATTTAC	2350
TTTGTTCATA	GCTAAAGCCA	CCGACC ACTG	CTTCAATCGC	ACCATTATCT	2400
GAATTAAAGAG	AAACTAATGC	TGAATTGCT	GCGGGAATTT	GTCCTAATTG	2450
CCATTCCCCA	TTAGCAGC GCT	GATGAATCCA	AATTGCTCG	CCGACTTTCA	2500
CAGGATTGCT	TCTGCCTGTC	CAACGCATTG	CATTGGTTGA	TAAGGT CATT	2550
TTTTCCCCAG	AAGCGAGCAA	TATATCAGCA	CCGCCTTTTA	CAATTCCAAT	2600
CACTGCCGCA	GGAATAAAATG	GCTCTGAATC	AGGTAGTTG	CGTAGAAAAC	2650
CGACAATGCG	ATCATTGTC	CAAGCGGTT	CATTTTTTG	CCATAATGGC	2700
GCGCCACCGC	GATAACCGTG	ACGCATATCG	TAATCAATCA	AGTTATTACG	2750
CACAGCTTTT	TGGGCTTCAG	CTTGGTCTTT	TGAAAGTACA	GTGGTAAATA	2800
CTTTATAACC	ACTGGTGTAA	GCATTTCTT	CGCCAAAACG	ACGCACCATT	2850
TCTTGACGCA	CCATTTCA GT	GACATAATCG	GCTCGAAATT	CAAATTTGC	2900
GCCGTGATAG	CTCGCCACAA	TCGGCTCTT	CAATGCAGCA	TCATATTCTT	2950
CTTTGCTGAT	GTATTTTCA	TCTAACATAC	GGCTTAGCAC	CACATTGCGG	3000
CGTTCTTCTG	AACGTTTAA	AGAATAAAGC	GGGTTCATTG	TTGAAGGTGC	3050
TTTAGGTAAA	CCAGCAATAA	TCGCCATTTC	CGATAAGGTC	AATTCAATTCA	3100
ATGATTTACC	GAAATAGGTT	TGTGCTGCCG	CTGCAACACCC	ATAAGAACGA	3150
TAGCCTAAAA	AGATTTGTT	TAAATAAAGC	TCTAATATTT	CTTGGTTGTT	3200
GAGAGTATTT	TCGATTTCTA	CCGCAAGCAC	GGCTTCACGA	GCTTACGAA	3250
TAATGGTTTT	TTCTGAGGTT	AAGAAAAGT	TACCGCCTAA	TTGTTGAGTA	3300
ATCGTACTTG	CGCCTTGTGA	TGCACCGCCA	TTACTCACTG	CGACAAACAA	3350
TGCACGGGCA	ATGCCGATAG	GGTCTAATCC	GTGATGATCG	AAAAAACGAC	3400
TGTCTTCCGT	CGCTAAAAAT	GGTCAATT	AGCGTTGTGG	CACATCGGCT	3450
AATTCACTG	GAATACGGCG	TTGCTCACCC	ACTTCGCCAA	TTAATTTACC	3500
GTCAGCCGTA	AAAATCTGCA	TTGGTTGCTG	TAATTCAACG	GTTTTTAATG	3550
TTTCTACTGA	GGGCAATTCA	GATTITAAGT	GGAAATACAA	CATTCCGCCT	3600
GCTACTAAC	CTAAAATACA	TAAAGTTAAT	AGGGTGT TTA	ATATTAATTT	3650
TGCGATCCGC	ATCGTAAAAT	TCTCGCTTCG	TTAATGAATA	TTCTTGTCAA	3700
GAGACCTATG	ATTTGGCTGT	TAAGTATAAA	AGATTCAGCC	TTTAAAGAAT	3750
AGGAAAGAAT	ATGCAATTCT	CCCTGAAAAA	TTACCGCACT	TTACAAATCG	3800
GCATTCACTG	TAAGCAGAGT	TATTTGATT	TTGTGTGGTT	TGATGATCTC	3850

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GAACAGCCAC	AAAGTTATCA	AATCTTTGTT	AATGATCGTT	ATTTTAAAAA	3900
TCGTTTTTA	CAACAGCTAA	AAACACAATA	TCAAGGGAAA	ACCTTCCTT	3950
TGCAGTTGT	AGCAAGCATT	CCCGCCCCT	TAACCTGGTC	GAAAGTATTA	4000
ATGTTGCCAC	AAGTGTAAA	TGCGCAAGAA	TGTCATCAAC	AATGTAAATT	4050
TGTGATTGAA	AAAGAGCTGC	CTATTTTTT	AGAAGAATTG	TGGTTTGATT	4100
ATCGTTCTAC	CCCGTTAAAG	CAAGGTTTC	GATTAGAGGT	TACTGCAATT	4150
CGTAAAAGTA	GCGCTAAAC	TTATTTGCAA	GATTTTCAGC	CATTTAATAT	4200
TAATATATTG	GATGTTGCGT	CAAATGCTGT	TTTGCCTGCA	TTTCAATATC	4250
TGTTGAATGA	ACAAGTGGGG	TCAGAAAATA	CCTTATTTTT	ATTTCAAGAA	4300
GATGACTATT	GCTTGGCGAT	TTGTGAAAGA	TCTCAGCAAT	CACAAATTTT	4350
ACAATCTCAC	AAAAATTGAA	CCGCACTTA	TGAACAATT	ACCGAACGTT	4400
TTGAAGGACA	ACTTGAACAA	GTTTTGTTT	ATCAAATTCC	CTCAAGTCAT	4450
ACACCATTAC	CCGAAAACGT	GCAGCGAGTA	GAAACAGAAC	TCCCTTTAT	4500
TGCGCTGGGC	AACCGCCTAT	GGCAAAAAGA	TTTACATCAA	CAAAAAGTGG	4550
GTGGTTAAAT	GTCGATGAAT	TTATTGCCTT	GGCGTACTTA	TCAACATCAA	4600
AAGCGTTTAC	GTCGTTTACG	TTTTTATATC	GCTTTATTTA	TCTTGCTTGC	4650
TATTAATTAA	ATGTTGGCTT	TTAGCAATT	GATTGAACAA	CAGAAACAAA	4700
ATTTGCAGGC	ACAGCAAAAG	TCGTTGAAC	AACTTAATCA	ACAGCTTCAT	4750
AAAACCTACCA	TGCAAATTGA	TCAGTTACGC	ATTGCGGTGA	AAGTTGGTGA	4800
AGTTTTGACA	TCTATTCCC	ACGAGCAAGT	AAAAAAAGAGT	TTACAACAGC	4850
TAAGTGAATT	ACCTTTCAA	CAAGGAGAAC	TGAATAAATT	TAAACAAGAT	4900
GCCAATAACT	TAAGCTTGG	AGGTAACGCG	CAAGATCAA	CAGAATTGAA	4950
ACTGATTCA	CAATTTTAA	AGAAACATT	TCCCAATGTG	AAATTAAGTC	5000
AGGTTCAACC	TGAACAAGAT	ACATTGTTT	TTCACTTGA	TGTGGAACAA	5050
GGGGCGGAAA	AATGAAAGCT	TTTTTTAACG	ATCCTTTAC	TCCTTTGGAA	5100
AAATGGCTAA	GTCAGCCTT	TTATGTGCAC	GGTTTAACCT	TTTTATTGCT	5150
ATTAAGTGCG	GTGATTTTC	GCCCCGTTT	AGATTATATA	GAGGGGAGTT	5200
CACGTTCCA	TGAAATTGAA	AATGAGTTAG	CGGTGAAACG	TTCAGAATTG	5250
TTGCATCAAC	AGAAAATT	AACCTCTTA	CAACAGCAGT	CGGAAAGTCG	5300
AAAACTTCT	CCAGAACTGG	CTGCACAAAT	TATTCCCTTG	AATAAACAAA	5350
TTCAACGTT	AGCTGCGCGT	AACGGTTTAT	CTCAGCATTT	ACGTTGGGAA	5400
ATGGGGCAAA	AGCCTATT	GCATTTACAG	CTTACAGGTC	ATTTTGAAAA	5450
AACGAAGACA	TTTTTATCCG	CACTTTGGC	TAATTCGTCA	CAGCTTCTG	5500
TAAGTCGGTT	GCAATTATG	AAACCCGAAG	ACGGCCCATT	GCAAACCGAG	5550
ATCATTTC	AGCTAGATAA	GGAAAACAAA	TGAAACATTG	GTTTTCTCTG	5600
ATTATATTAT	TTTTTATGAA	TTGCAGTTGG	GGACAAGATC	CTTCGATAAA	5650
AACACAGCGT	AACCCTCTC	AGTTTGATAA	CGCACAAACA	GTAATGGAGC	5700

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AAACAGAAAT	AATTCCTCA	GATGTGCCTA	ATAATCTATG	CGGAGCGGAT	5750
GAAAATCGCC	AAGCGGCTGA	AATTCCCTTG	AACGCTTTAA	AATTGGTGGG	5800
GGTAGTGATT	TCTAAAGATA	AAGCCTTGC	CTTGTGTC	GATCAAGGTT	5850
TGCAAGTTA	CAGCGTTTA	GAGGGCGTTG	ATGTGGCTCA	AGAGGGCTAT	5900
ATTGTAGAAA	AAATCAACCA	AAACAATGTT	CAATTATGCC	GTAAGCTAGG	5950
AGAGCAATGT	GATAGTAGTG	AATGGAAAAA	ATTAAGTTTT	TAAAGGAAGA	6000
TTATGAAGAA	ATATTTTTA	AAGTGCCTT	ATTTTTAGT	ATGTTTTGT	6050
TTGCCATTAA	TCGTTTTGC	TAATCCTAAA	ACAGATAACG	AACGTTTTT	6100
TATTCGTTA	TCGCAAGCAC	CTTTAGCTCA	AACACTGGAG	CAATTAGCTT	6150
TTCAACAAGA	TGTGAATT	GTGATTGGAG	ATATATTGGA	AAACAAGATC	6200
TCTTGAAAT	TAAACAATAT	TGATATGCCA	CGTTTGCTAC	AAATAATCGC	6250
AAAAAGTAAG	CATCTTACTT	TGAATAAAAGA	TGATGGGATT	TATTATTTAA	6300
ACGGCAGTCA	ATCTGGCAAA	GGTCAGGTG	CAGGAAATCT	TACGACAAAT	6350
GAACCGCACT	TAGTGAGTCA	CACGGTAAAA	CTCCATTTG	CTAAAGCTTC	6400
TGAATTAATG	AAATCCTTAA	CAACAGGAAG	TGGCTCTTG	CTTTCTCCCG	6450
CTGGGAGCAT	TACCTTGAT	GATCGCAGTA	ATTTGCTGGT	TATTCAAGGAT	6500
GAACCTCGTT	CTGTGCAAAA	TATCAAAAAA	CTGATTGCTG	AAATGGATAA	6550
GCCTATTGAA	CAGATCGCTA	TTGAAGCGCG	AATTGTGACA	ATTACGGATG	6600
AGAGTTTGAA	AGAACTTGGC	GTTCGGTGGG	GGATTTTTAA	TCCAAGTGAA	6650
AATGCAAGAC	GAGTTGCGGG	CAGCCTTACA	GGCAATAGCT	TTGAAAATAT	6700
TGCGGATAAT	CTTAATGTAA	ATTTGCGAC	AACGACGACA	CCTGCTGGCT	6750
CTATAGCATT	ACAAGTCGCC	AAAATTAATG	GGCGATTGCT	TGATTTAGAA	6800
TTGAGTGCCT	TGGAGCGTGA	AAATAATGTA	GAAATTATTG	CAAGCCCTCG	6850
CTTACTCACT	ACCAATAAGA	AAAGTGCAG	CATTAACAG	GGGACAGAAA	6900
TTCCTTACAT	CGTGAGTAAT	ACTCGTAACG	ATACGCAATC	TGTGGAATT	6950
CGTGAGGCCG	TGCTTGGTT	GGAAGTGACG	CCACATATT	CTAAAGATAA	7000
CAATATCTTA	CTTGATTAT	TGGTAAGTCA	AAATTCCCT	GGTTCTCGTG	7050
TCGCTTATGG	ACAAAATGAG	GTGGTTCTA	TTGATAAAACA	AGAAAATTAAT	7100
ACTCAGGTTT	TTGCCAAAGA	TGGGGAAACC	ATTGTGCTTG	GCGCGTATT	7150
TCACGATACA	ATCACGAAAA	GCGAAGATAA	AGTGCCATTG	CTTGGCGATA	7200
TACCCGTTAT	TAAACGATTA	TTAGCAAAG	AAAGTGAACG	ACATCAAAAA	7250
CGTGAGCTAG	TGATTTTCGT	CACGCCACAT	ATTTAAAAG	CAGGAGAAAA	7300
CGTTAGAGGC	GTTGAAACAA	AAAAGTGAGG	GTAAAAAATA	ACTTTTAAA	7350
TGATGAATT	TTTAATTTT	CGCTGTATCC	ACTGTCGTGG	CAATCTTCAT	7400
ATCGCAAAAA	ATGGGTTATG	TTCAAGGTTGC	CAAAAACAAA	TTAAATCTT	7450
TCCTTATTGC	GGTCATTGTG	GTTCGGAATT	GCAATTATTAT	GCGCAGCATT	7500
GTGGGAATTG	TCTTAAACAA	GAACCAAGTT	GGGATAAGAT	GGTCATTATT	7550

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GGGCATTATA	TTGAACCTCT	TTCGATATTG	ATTCAGCGTT	TTAAATTC	7600
AAATCAATTT	TGGATTGACC	GCACTTAGC	TCGGCTTTA	TATCTTGC	7650
TACGTGATGC	TAAACGAACG	CATCAACTTA	AATTGCCAGA	GGCAATCATT	7700
CCAGTGCCTT	TATATCATT	TCGTCAGTGG	CGACGGGTT	ATAATCAGGC	7750
AGATTTATTA	TCTCAGCAAT	TAAGTCGTTG	GCTGGATATT	CCTAATTG	7800
ACAATATCGT	AAAGCGTGTG	AAACACACCT	ATACTCAACG	TGGTTTGAGT	7850
GCAAAAGATC	GTCGTCAGAA	TTTAAAAAAT	GCCTTTCTC	TTGCTGTTTC	7900
GAAAAATGAA	TTTCCTTATC	GTCGTGTTGC	GTTGGTGGAT	GATGTGATTA	7950
CTACTGGTTC	TACACTCAAT	GAAATCTCAA	AATTGTTGCG	AAAATTAGGT	8000
GTGGAGGAGA	TTCAAGTGTG	GGGGCTGGCA	CGAGCTTAAT	ATAAAAGCACT	8050
GGAAAAAAA	GCGCGATAAG	CGTATTATTC	CCGATACTTT	CTCTCAAGTA	8100
TTTAGGACAT	AATTATGGAA	CAAGCAACCC	AGCAAATCGC	TATTTCTGAT	8150
GCCGCACAAG	CGCATTTCG	AAAACTTTA	GACACCCAAG	AAGAAGGAAC	8200
GCATATTCGT	ATTTTCGCGG	TTAACCTTGG	TACGCCTAAT	GCGGAATGTG	8250
GCGTATCTTA	TTGCCCCCCG	AATGCCGTGG	AAGAAAGCGA	TATTGAAATG	8300
AAATATAATA	CTTTTCTGC	ATTTATTGAT	GAAGTGAAGTT	TGCTTTCTT	8350
AGAAGAAGCA	GAAATTGATT	ATGTTACCGA	AGAGCTTGGT	GCGCAACTGA	8400
CCTTAAAAGC	ACCGAATGCC	AAAATGCGTA	AGGTGGCTGA	TGATGCGCCA	8450
TTGATTGAAC	GTGTTGAATA	TGTAATTCAA	ACTCAAATTA	ACCCACAGCT	8500
TGCAAATCAC	GGTGGACGTA	TAACCTTAAT	TGAAAATTACT	GAAGATGGTT	8550
ACCGAGTTT	ACAATTGGT	GGTGGCTGTA	ACGGTTGTT	AATGGTGGAT	8600
GTTACGTTAA	AAGATGGGGT	AGAAAAACAA	CTTGTAGCT	TATTCCCGAA	8650
TGAATTAAA	GGTGCAAAAG	ATATAACTGA	GCATCAACGT	GGCGAACATT	8700
CTTATTATTA	GTGAGTTATA	AAAGAAGATT	TATAATGACC	GCACCTTTGA	8750
AAGTGCGGTT	ATTTTATGG	AGAAAAAATG	AAAATACTTC	AACAAGATGA	8800
TTTGGTTAT	TGGTTGCTTA	CACAAGGTT	TAATCTGTAT	TTAGTGAATA	8850
ATGAATTGCC	TTTTGGTATC	GCTAAAGATA	TTGATTGGA	AGGATTGCAG	8900
GCAATGCAA	TTGGGGAAATG	GAAAAATTAT	CCGTTGTGGC	TTGTGGCTGA	8950
GCAAGAAAGT	GATGAACGAG	AATATGTGAG	TTTGAGTAAC	TTGCTTTCAC	9000
TGCCAGAGGA	TGAATTCCAT	ATATTAAGCC	GAGGTGTGGA	AATTAATCAT	9050
TTTCTGAAAA	CCCATAAAATT	CTGTGGAAAG	TGCGGTCTATA	AAACACAAACA	9100

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

AAAAATCGAC	TGCCGTCATT	TTCAACCACC	ACATAGCTCA	TATTCGCAAG	50
CCAATGTATT	GACCGTTGGG	AATAATAACA	GCCCCAAAAC	AATGAAACAT	100
ATGGTGATGA	GCCAAACATA	CTTCCCTGCA	GATTTGGAA	TCATATCGCC	150
ATCAGCACCA	GTATGGTTG	ACCAAGTATTT	AACGCCATAG	ACATGTGTAA	200
AAAAATTAAA	TAACGGTGCA	AGCATGAGAC	CAACGGCACC	TGATGTACCT	250
TGTACGATGA	CCTCACCTGC	TGTGGCAACC	ATACCAAGTC	CATTGCCTGT	300
GATATTTTTG	CGAAAAGACA	AACTTACAC	ACAGACCAAG	CCGATGATTG	350
AGATGACAAA	ATAAAACCAA	TCCAAATGCG	TGTGAGCTGT	TGTGGTCAA	400
AATCCAGTAA	ATAGTGCAAT	AAATCCGCAA	ACAAACCAAA	GTAGCACCCA	450
GCTTGTGTC	CAATCTTTT	TACCAAAGCC	TGTGATGTTA	TCTAAAATAT	500
CAATTTTCAT	CAGATTTCC	CTAAT			525

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TAATGATAAC	CAGTCAAGCA	AGCTCAAATC	AGGGTCAGCC	TGTTTTGAGC	50
TTTTTATTTT	TTGATCATCA	TGCTTAAGAT	TCACTCTGCC	ATTTTTTTAC	100
AACCTGCACC	ACAAGTCATC	ATCGCATTG	CAAAAATGGT	ACAAACAAGC	150
CGTCAGCGAC	TTAAACAAAA	AAAGGCTCAA	TCTGCGTGTG	TGGGTTCACT	200
TTTACAAATC	ACCATGCACC	GCTTGTACAT	TGTTGGTGA	TTTCATGACC	250
ATGCACACCC	TTATTATATT	AACTCAAATA	AAATACGCTA	CTTTGTCAGC	300
TTTAGCCATT	CAGATAATCA	AGTCGCTCTC	ATCATCAGCT	TAACACCTTG	350
TGCCATTGAC	ATAGAAGTTA	ACGATATTAA	ATACAGTGTG	GTTGAACGAT	400
ACTTTCATCC	CAATGAAATT	TATCTACTTA	CTCAATTAG	CTCTACTGAT	450
AGGCAACAGC	TTATTA				466

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(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 631 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GATCTTGAT	TTTCATTGAG	TATTACTCTC	TCTTGTCACT	TCTTTCTATT	50
TTACCATAAA	GTCCAGCCTT	TGAAGAACCTT	TTACTAGAACG	ACAAGGGGCT	100
TCTGTCTCTA	TTTGCATCT	TAGGCATCAA	AAAAGAGGGG	TCATCCCTCT	150
TTACGAATTTC	AATGCTACTA	GGGTATCCAA	ATACTGGTTG	TTGATGACTG	200
CCAAAATATA	GGTATCTGCT	TTCAAGAGGT	CATCTGGTCC	AAATTCAACA	250
TCCAATGGGG	AATTTCCTG	CTCTCGGAAA	CCCAAAATAT	TCAGATTGTA	300
TTTGCCACGG	AGGTCTAATT	TACTTCAGAC	TTTGACCTGC	CCAAGACTGA	350
GGAATTTCA	TCTCCACGAT	AGACACATTT	TTATCCAATC	GAAAGACATC	400
AACACTATTA	TGAAAAGAAT	GGTCTGTGCT	AGAGACTGCC	CCATTTCATA	450
CTCTGGCGAG	ATAACCGAGT	CAGCTCCAAT	CTTTTCTAGC	ACTTTCTTAG	500
CGGTCTGACT	TTTGACCTTA	GCAATAACAG	TCGGTACCCC	CAAACCTTTA	550
CAGTGCATAA	CCGCAAGCAC	ACTCGACTCC	AGATTTTCAC	CTGTCGCGAC	600
TACAACGGTA	TCGCAGGTAT	CAATCCCTGC	T		631

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3754 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CCAATATTTT	GGTCAGCATA	GTGTTCTTT	TCAGTGGTAA	CAGCTTGCAA	50
TACTTGAGCA	GAAATGGCAG	ATTTATCAAG	AAAAAAAGTTA	ACGTAAGGTC	100

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CTGTTGCGAC	AACTTTTCA	AAGGCTTGGC	TGTTCATTTT	TTCAGCCAGT	150
TCAGCCGCAA	TCATTGTGG	TGCTTTACGT	TCGACTTTTG	CAAGAGAAAA	200
AGCAGGGAAA	GCAATGTCTC	CCATTTCTGA	GTFFFFTAGGG	GTTCAGCTA	250
ACTTTAAAAT	AGCCTCTTGG	TCCAGGCTAT	CAATGATGCT	AGATAATTG	300
CTAGCAATCA	ATTCTTTGT	ATTCAATTAAAG	AGCTCCTTTT	TGGACTTTTC	350
TACTATTTA	TCACAATTAA	AAAGAAAGAA	GAAGAAATTAA	TTGAAATCTC	400
CTGTTTTTTT	GGTATAATAT	GGTTATAAAAT	ATAGTTATAAA	ATATAGTTAT	450
AAATATGCAC	GCAAGAGGAT	TTTATGAGAA	AAAGAGATCG	TCATCAGTTA	500
ATAAAAAAA	TGATTACTGA	GGAGAAATTAA	AGTACACAAA	AAGAAATTCA	550
AGATCGGTTG	GAGGCGCACA	ATGTTTGTGT	GACGCAGACA	ACCTTGTCTC	600
GTGATTTGCG	CGAAATCGGC	TTGACCAAGG	TCAAGAAAAA	TGATATGGTG	650
TATTATGTAC	TAGTAAATGA	GACAGAAAAG	ATTGATTTGG	TGGAATTTTT	700
GTCTCATCAT	TTAGAAGGTG	TTGCAAGAGC	AGAGTTTACC	TTGGTGTCTC	750
ATACCAAATT	GGGAGAAGCC	TCTGTTTGG	CAAATATTGT	AGATGTAAAC	800
AAGGATGAAT	GGATTTAGG	AACAGTTGCT	GGTGCCAATA	CCTTATTGGT	850
TATTTGTCGA	GATCAGCACG	TTGCCAAACT	CATGGAAGAT	CGTTTGCTAG	900
ATTTGATGAA	AGATAAGTAA	GGTCTTGGGA	GTTGCTCTCA	AGACTTATTT	950
TTGAAAAGGA	GAGACAGAAA	ATGGCGATAG	AAAAGCTATC	ACCCGGCATG	1000
CAACAGTATG	TGGATATTAA	AAAGCAATAT	CCAGATGCTT	TTTGCTCTT	1050
TCGGATGGGT	GATTTTTATG	AATTATTATA	TGAGGATGCG	GTCAATGCTG	1100
CGCAGATTCT	GGAAATTTC	TTAACGAGTC	GCAACAAGAA	TGCCGACAAT	1150
CCGATCCCTA	TGGCGGGTGT	TCCCTATCAT	TCTGCCAAC	AGTATATCGA	1200
TGTCTTGATT	GAGCAGGGTT	ATAAGGTGGC	TATCGCAGAG	CAGATGGAAG	1250
ATCCTAAACA	AGCAGTTGGG	GTTGTTAAC	GAGAGGTTGT	TCAGGTCATT	1300
ACGCCAGGGA	CAGTGGTCGA	TAGCAGTAAG	CCGGACAGTC	AGAATAATT	1350
TTTGGTTTCC	ATAGACCGCG	AAGGCAATCA	ATTTGGCCTA	GCTTATATGG	1400
ATTTGGTGAC	GGGTGACTTT	TATGTACAG	GTCTTTGG	TTTCACGCTG	1450
GTTTGTGGGG	AAATCCGTAA	CCTCAAGGCT	CGAGAAGTGG	TGTTGGGTTA	1500
TGACTTGTCT	GAGGAAGAAG	AAACAAATCCT	CAGCCGCCAG	ATGAATCTGG	1550
TACTCTCTTA	TGAAAAAGAA	AGCTTGAAG	ACCTTCATTT	ATTGGATTTG	1600
CGATTGGCAA	CGGTGGAGCA	AACGGCATCT	AGTAAGCTGC	TCCAGTATGT	1650
TCATCGGACT	CAGATGAGGG	AATTGAACCA	CCTCAAACCT	GTTATCCGCT	1700
ACGAAATTAA	GGATTTCTTG	CAGATGGATT	ATGCGACCAA	GGCTAGTCTG	1750
GATTTGGTTG	AGAATGCTCG	CTCAGGTAAG	AAACAAGGCA	GTCTTTCTG	1800
GCTTTGGAT	GAAACCAAAA	CGGCTATGGG	GATGCGTCTC	TTGCGTTCTT	1850
GGATTCACTCG	CCCCCTGATT	GATAAGGAAC	GAATCGTCCA	ACGTCAAGAA	1900
GTAGTGCAGG	TCTTTCTCGA	CCATTCTTT	GAGCGTAGTG	ACTTGACAGA	1950

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CAGTCTCAAG	GGTGTATG	ACATTGAGCG	CTTGGCTAGT	CGTGTTC	2000
TTGGCAAAAC	CAATCCAAAG	GATCTCTGC	AGTTGGCGAC	TACCTTG	2050
AGTGTGCCAC	GGATTCGTGC	GATTTAGAA	GGGATGGAGC	AACCTACTCT	2100
AGCCTATCTC	ATCGCACAAC	TGGATGCAAT	CCCTGAGTTG	GAGAGTTGA	2150
TTAGCGCAGC	GATTGCTCCT	GAAGCTCCTC	ATGTGATTAC	AGATGGGGGA	2200
ATTATCCGGA	CTGGATTTGA	TGAGACTTTA	GACAAGTATC	GTTGCGTTCT	2250
CAGAGAAGGG	ACTAGCTGGA	TTGCTGAGAT	TGAGGCTAAG	GAGCGAGAAA	2300
ACTCTGGTAT	CAGCACGCTC	AAGATTGACT	ACAATAAAA	GGATGGCTAC	2350
TATTTTCATG	TGACCAATTG	GCAACTGGGA	AATGTGCCAG	CCCAC	2400
CCGCAAGGCG	ACGCTGAAAA	ACTCAGAACG	CTTTGGAACC	GAAGAATTAG	2450
CCCGTATCGA	GGGAGATATG	CTTGAGGCGC	GTGAGAAGTC	AGCCAACCTC	2500
GAATACGAAA	TATTTATGCG	CATTCGTGAA	GAGGTGGCA	AGTACATCCA	2550
GCGTTACAA	GCTCTAGCCC	AAGGAATTGC	GACGGTTGAT	GTCTTACAGA	2600
GTCTGGCGGT	TGTGGCTGAA	ACCCAGCATT	TGATTCGACC	TGAGTTGGT	2650
GACGATTCA	AAATTGATAT	CCGGAAAGGG	CGCCATGCTG	TCGTTGAAA	2700
GGTTATGGGG	GCTCAGACCT	ATATTCCAAA	TACGATTTCAG	ATGGCAGAAG	2750
ATACCACTAT	TCAATTGGTT	ACAGGGCCAA	ACATGAGTGG	GAAGTCTACC	2800
TATATGCGTC	AGTTAGCCAT	GACGGCGGTT	ATGGCCCAGC	TGGGTTCC	2850
TGTTCTGCT	GAAAGCGCCC	ATTTACCGAT	TTTGATGCG	ATTTTACCC	2900
GTATCGGAGC	AGCAGATGAC	TTGGTTTCGG	GTCAGTCAAC	CTTTATGGTG	2950
GAGATGATGG	AGGCCAATAA	TGCCATTTCG	CATGCGACCA	AGAACTCTCT	3000
CATTCTCTT	GATGAATTGG	GACGTGGAAC	TGCAACTTAT	GACGGGATGG	3050
CTCTTGTCA	GTCCATCATC	GAATATATCC	ATGAGCACAT	CGGAGCTAAG	3100
ACCCCTTTG	CGACCCACTA	CCATGAGTTG	ACTAGTCTGG	AGTCTAGTTT	3150
ACAACACTTG	GTCAATGTCC	ACGTGGCAAC	TTTGGAGCAG	GATGGGCAGG	3200
TCACCTTCCT	TCACAAGATT	GAACCGGGAC	CAGCTGATAA	ATCCTACGGT	3250
ATCCATGTTG	CCAAGATTGC	TGGCTTGCCA	GCAGACCTTT	TAGCAAGGGC	3300
GGATAAGATT	TTGACTCAGC	TAGAGAATCA	AGGAACAGAG	AGTCCTCCTC	3350
CCATGAGACA	AACTAGTGCT	GTCACTGAAC	AGATTTCACT	CTTGATAGG	3400
GCAGAAGAGC	ATCCTATCCT	AGCAGAATTA	GCTAAACTGG	ATGTGTATAA	3450
TATGACACCT	ATGCAGGTTA	TGAATGTCTT	AGTAGAGTTA	AAACAGAAC	3500
TATAAAACCA	AGACTCACTA	GTAAATCTAG	CTGTATCAAG	GAGACTTCTT	3550
TGACAATTCT	CCACTTTTT	GCTAGAATAA	CATCACACAA	ACAGAATGAA	3600
AAGGGCTGAC	GCATTGTCGC	TCCCTTTGT	CTATTTTTA	AGGAGAAAGT	3650
ATGCTGATTG	AGAAAATAAA	AACCTACAAG	TGGCAGGCC	TGCTTCGCTC	3700
CTGATGACAG	GCTTGATGGT	TGCTAGTTCA	CTTCTGCAAC	CGCGTTATCT	3750
GCAG					3754

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(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1337 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

AACAAAATAA	AAGAACTTAC	CTATTTCCA	TCCAAAATGT	TTAGCAATCA	50
TCATCTGCAA	GGCAACGTAT	TGCATGGCAT	TGATGTGATG	AGCAACTAAT	100
ATGTCATTAG	AACGTTGCGT	CAAACTAGCA	TCTAAATAAA	GATCGAAATG	150
CAGTTATCAA	AAATGCAAGC	TCCTATCGGC	CCTTGTTTTA	ATTATTACTC	200
ACATTGCCCT	AATGTATTAA	CTTGCTTATT	ATTAACTTTT	TTGCTAAGTT	250
AGTAGCGTCA	GTTATTCCATT	GAAAGGACAT	TATTATGAAA	ATTCTTGTAA	300
CAGGCTTTGA	TCCCTTGGC	GGCGAAGCTA	TTAACCTCTGC	CCTTGAAGCT	350
ATCAAGAAAT	TGCCAGCAAC	CATTATGGA	GCAGAAATCA	AATGTATTGA	400
AGTTCCAACG	GTTCCTCAAA	AATCTGCCGA	TGTGCTCCAG	CAGCATATCG	450
AAAGCTTTCA	ACCTGATGCA	GTCCTTGTA	TTGGGCAAGC	TGGTGGCCGG	500
ACTGGACTAA	CGCCAGAACG	CGTTGCCATT	AATCAAGACG	ATGCTCGCAT	550
TCCTGATAAC	GAAGGGAATC	AGCCTATTGA	TACACCTATT	CGTGCAGATG	600
GTAAAGCAGC	TTATTTTCA	ACCTTGCCAA	TCAAAGCGAT	GGTTGCTGCC	650
ATTCAATCAGG	CTGGGCTTCC	TGCTTCTGTT	TCTAACACAG	CTGGTACCTT	700
TGTTTGCAAT	CATTGATGT	ATCAAGCCCT	TTACTTAGTG	GATAAATATT	750
GTCCAAATGC	CAAAGCTGGG	TTTATGCATA	TTCCCTTTAT	GATGGAACAG	800
GTTGTTGATA	AACCTAACAC	AGCTGCCATG	AACCTCGATG	ATATTACAAG	850
AGGAATTGAG	GCTGCTATTT	TTGCCATTGT	CGATTCAAA	GATCGTTCCG	900
ATTTAAAACG	TGTAGGGGGC	GCTACTCACT	GACTGTGACG	CTACTAAACC	950
TATTTTAAAA	AAACAGAGAT	ATGAACTAAC	TCTGTTTTTT	TTGTGCTAAA	1000
AATGAAAGAC	CTAGGGAAAC	TTTCATCGG	TCTTTCTCAA	TTGTCATCTT	1050
AATCTAACAC	TACTTCTAAC	ATCAGCGGGT	ATAGTTTGCC	AGTAATTAAG	1100
AAACGTTGTT	GATCTAAATG	AGCAATCCCA	TTCAAAACAT	TAAGGTCAGG	1150
GTAATGGGAC	TTATCAAGAT	TTAAGGCTTT	TAACAAAGGA	CTAATATCAT	1200
AGGTGGCTAC	CACCTTTCCA	GAATCAGGTT	GGAGTTTGAC	AATAGTATTG	1250
GTTTGCCAAA	TATGGCATA	GAGATAACCA	TCTACATACT	CTAATTGTT	1300
AAGCATTGAG	ATAGGGACAC	TTTCTATAGC	AACTAGT		1337

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(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1837 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TCATGTTGA	CAGCTTATCA	TCGATAAGCT	TACTTTCGA	ATCAGGTCTA	50
TCCTTGAAC	AGGTGCAACA	TAGATTAGGG	CATGGAGATT	TACCAAGACAA	100
CTATGAACGT	ATATACTCAC	ATCACGCAAT	CGGCAATTGA	TGACATTGGA	150
ACTAAATTCA	ATCAATTGT	TACTAACAAAG	CAACTAGATT	GACAACATAAT	200
TCTCAACAAA	CGTTAATTAA	ACAACATTCA	AGTAACCTCC	ACCAGCTCCA	250
TCAATGCTTA	CCGTAAGTAA	TCATAACTTA	CTAAAACCTT	GTTACATCAA	300
GGTTTTTCT	TTTTGTCTTG	TTCATGAGTT	ACCATAACTT	TCTATATTAT	350
TGACAACATAA	ATTGACAAC	CTTCAATTAT	TTTCTGTCT	ACTCAAAGTT	400
TTCTTCATTT	GATATAGTCT	AATTCCACCA	TCACTTCTTC	CACTCTCTCT	450
ACCGTCACAA	CTTCATCATC	TCTCACTTT	TCGTGTGGTA	ACACATAATC	500
AAATATCTTT	CCGTTTTAC	GCACATATCGC	TACTGTGTCA	CCTAAAATAT	550
ACCCCTTATC	AATCGCTTCT	TTAAACTCAT	CTATATATAA	CATATTTCAT	600
CCTCCTACCT	ATCTATTCTG	AAAAAGATAA	AAATAACTAT	TGTTTTTTTT	650
GTTATTTAT	AATAAAATTA	TTAATATAAG	TTAATGTTT	TTAAAAATAT	700
ACAATTTAT	TCTATTTATA	GTTAGCTATT	TTTCATTGT	TAGTAATATT	750
GGTGAATTGT	AATAACCTTT	TTAAATCTAG	AGGAGAACCC	AGATATAAAA	800
TGGAGGAATA	TTAATGGAAA	ACAATAAAA	AGTATTGAAG	AAAATGGTAT	850
TTTTGTTTT	AGTGACATT	CTTGGACTAA	CAATCTCGCA	AGAGGTATTT	900
GCTCAACAAG	ACCCCGATCC	AAGCCAACCT	CACAGATCTA	GTTCAGTTAA	950
AAACCTTCAA	AATATATATT	TTCTTTATGA	GGGTGACCC	GTTACTCAG	1000
AGAATGTGAA	ATCTGTTGAT	CAACTTTAT	CTCACGATT	AATATATAAT	1050
GTTTCAGGGC	CAAATTATGA	TAAATTAAA	ACTGAACCTA	AGAACCAAGA	1100
GATGGCAACT	TTATTTAAGG	ATAAAAACGT	TGATATTAT	GGTGTAGAAT	1150
ATTACCATCT	CTGTTATTAA	TGTGAAAATG	CAGAAAGGAG	TGCATGTATC	1200
TACGGAGGGG	TAACAAATCA	TGAAGGGAAT	CATTTAGAAA	TTCCCTAAAAA	1250
GATAGTCGTT	AAAGTATCAA	TCGATGGTAT	CCAAAGCCTA	TCATTTGATA	1300

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TTGAAACAAA	AAAAAAATG	GTAAGTGTCT	AAGAATTAGA	CTATAAAGTT	1350
AGAAAATATC	TTACAGATAA	TAAGCAACTA	TATACTAATG	GACCTTCTAA	1400
ATATGAAACT	GGATATATAA	AGTTCATACC	TAAGAATAAA	GAAAGTTTTT	1450
GGTTTGATT	TTTCCCTGAA	CCAGAATTAA	CTCAATCTAA	ATATCTTATG	1500
ATATATAAAG	ATAATGAAAC	GCTTGACTCA	AACACAAGCC	AAATTGAAGT	1550
CTACCTAAC	ACCAAGTAAC	TTTTGCTTT	TGGCAACCTT	ACCTACTGCT	1600
GGATTAGAA	ATTTTATTGC	AATTCTTTA	TTAATGTAAA	AACCGCTCAT	1650
TTGATGAGCG	GTTTTGTCTT	ATCTAAAGGA	GCTTTACCTC	CTAATGCTGC	1700
AAAATTTAA	ATGTTGGATT	TTTGTATTTG	TCTATTGTAT	TTGATGGGTA	1750
ATCCCATT	TCGACAGACA	TCGTCGTGCC	ACCTCTAAC	CCAAAATCAT	1800
AGACAGGAGC	TTGTAGCTTA	GCAACTATTT	TATCGTC		1837

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

GATCAATATG	TCCAAGAAC	CACATGTTCC	TAAGACAAGA	GCTAACAGAC	50
TGGCCGTCAA	TAATAGTATT	GTTCTTTTTT	TCATCATTAC	TCCTTAAC	100
GTGTTTAACT	GATTAATTAG	CCAGTAAATA	GTTTATCTTT	ATTTACACTA	150
TCTGTTAAGA	TATAGTAAA	TGAAATAAGA	ACAGGACAGT	CAAATCGATT	200
TCTAACAAATG	TTTTAGAAGT	AGAGGTATAC	TATTCTAATT	TCAATCTACT	250
ATATTTGCA	CATTTTCATA	AAAAAAATGA	GAACTAGAAC	TCACATTCTG	300
CTCTCATT	TCGTTTCCC	GTTCTCCTAT	CCTGTTTTA	GGAGTTAGAA	350
AATGCTGCTA	CCTTTACTTA	CTCTCCTTTA	ATAAAGCCAA	TAGTTTTCA	400
GCTTCTGCCA	TAATAGTATT	GTTGTCCTGG	GTGCCAAATA	GTAAATTATT	450
TTTTAATCCT	GTGAGAGTCT	CTTTGGCATT	GGACTTGATA	ATTGGATTCT	500
GGATTTTTCC	AAGTAAATCT	TCAGCCTCTC	TCAGTTTCT	TAACCTTTCA	550
GTCTCGACCT	GAGGTCTTC	TGATTCCCTCT	GGTGATTCTT	CTGGTGATTC	600
TTCTTCTGGT	TCCTCTGTTG	GTTTGGAGA	CTCTGGTTTC	TCGCTTGCG	650
GTTCCTCTTC	TCGAGGGGTT	TCTTCCTCAG	GTTTTCTGT	CTGAGGTTTC	700
TCCTCGTTG	GTTTTCCGT	TTGATTGGTA	TCAGCTTGAC	CATTTTGT	750
TCTTGAACA	TGGTCGCTAG	CGTTACAAA	ACCATTATCT	GAATGCGACG	800

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TTCGTTGGA TGTCGACAT AGTACTTGAC AGTCGCCAAA A

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(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4500 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GATCAGGGACA	GTCAAATCGA	TTTCTAACAA	TGTTTAGAA	GTAGATGTGT	50
ACTATTCTAG	TTTCAATCTA	TTATATTTAT	AGAATTTTTT	GTTGCTAGAT	100
TTGTCAAATT	GCTTAAAATA	ATTTTTTC	GAAAGCAAAA	GCCGATACCT	150
ATCGAGTAGG	GTAGTTCTTG	CTATCGTCAG	GCTTGTCTGT	AGGTGTTAAC	200
ACTTTCAAA	AATCTCTTCA	AACAACGTCA	GCTTGCCTT	GCCGTATATA	250
TGTTACTGAC	TTCGTCAGTT	CTATCTGCCA	CCTCAAAACG	GTGTTTGAG	300
CTGACTTCGT	CAGTTCTATC	CACAACCTCA	AAACAGTGT	TTGAGCTGAC	350
TTCGTCAGTT	CTATCCACAA	CCTCAAAACA	GTGTTTGAG	CTGACTTTGT	400
CAGTCTTATC	TACAACCTCA	AAACAGTGT	TTGAGCATCA	TGCGGCTAGC	450
TTCTTAGTTT	GCTCTTGAT	TTTCATTGAG	TATAAAAACA	GATGAGTTTC	500
TGTTTTCTTT	TTATGGACTA	TAAATGTTCA	GCTGAAACTA	CTTTCAAGGA	550
CATTATTATA	TAAAAGAATT	TTTGAACACT	AAAATCTACT	ATATTACACT	600
ATATTGAAAG	CGTTTAAAAA	ATGAGGTATA	ATAAATTAC	TAACACTTAT	650
AAAAGTGT	AGAATCTATC	TTTATGTATA	TTTAAAGATA	GATTGCTGTA	700
AAAATAGTAG	TAGCTATGCG	AAATAACAGA	TAGAGAGAAG	GGATTGAAGC	750
TTAGAAAAGG	GGAATAATAT	GATATTAAAG	GCATTCAAGA	CAAAAAAGCA	800
GAGAAAAGA	CAAGTTGAAC	TACTTTGAC	AGTTTTTTC	GACAGTTTC	850
TGATTGATT	ATTTCTTCAC	TTATTTGGGA	TTGCCCCCTT	TAAGCTGGAT	900
AAGATTCTGA	TTGTGAGCTT	GATTATATT	CCCATTATT	CTACAAGTAT	950
TTATGCTTAT	AAAAAGCTAT	TTGAAAAGT	GTTCGATAAG	GATTGAGCAG	1000
GAAGTATGGT	GTAAAATAGCA	TAAGCTGATG	TCCATCATTT	GCTTATAAAG	1050
AGATATTTA	GTAAATTGC	AGCGGTGTCC	TGGTAGATAA	ACTAGATTGG	1100
CAGGAGTCTG	ATTGGAGAAA	GGAGAGGGGA	AATTGGCAC	CAATTGAGA	1150
TAGTTTGTTT	AGTCATT	TGTCATTTAA	ATGAACTGTA	GTAAAAGAAA	1200
GTTAATAAAA	GACAACTAA	GTGCATTTTC	TGGAATAAT	GTCTTATTTC	1250
AGAAATCGGG	ATATAGATAT	AGAGAGGAAC	AGTATGAATC	GGAGTGTTC	1300

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AGAACGTAAG	TGTCGTTATA	GCATTAGGAA	ACTATCGGTA	GGAGCGGTTT	1350
CTATGATTGT	AGGAGCAGTG	GTATTTGGAA	CGTCTCCTGT	TTTAGCTCAA	1400
GAAGGGCAA	GTGAGCAACC	TCTGGCAAAT	GAAACTCAAC	TTTCGGGGGA	1450
GAGCTCAACC	CTAACTGATA	CAGAAAAGAG	CCAGCCTTCT	TCAGAGACTG	1500
AACTTTCTGG	CAATAAGCAA	GAACAAGAAA	GGAAAGATAA	GCAAGAAGAA	1550
AAAATTCCAA	GAGATTACTA	TGCACGAGAT	TTGGAAAATG	TCGAAACAGT	1600
GATAGAAAAA	GAAGATGTTG	AAACCAATGC	TTCAAATGGT	CAGAGAGTTG	1650
ATTTATCAAG	TGAACTAGAT	AAACTAAAGA	AACTTGAAAA	CGCAACAGTT	1700
CACATGGAGT	TTAAGCCAGA	TGCCAAGGCC	CCAGCATTCT	ATAATCTCTT	1750
TTCTGTGTCA	AGTGCTACTA	AAAAAGATGA	GTACTTCACT	ATGGCAGTTT	1800
ACAATAATAC	TGCTACTCTA	GAGGGCGTG	GTTCGGATGG	GAAACAGTTT	1850
TACAATAATT	ACAACGATGC	ACCCTTAAAA	GTAAACCAG	GTCAGTGGAA	1900
TTCTGTGACT	TTCACAGTTG	AAAAACCGAC	AGCAGAACTA	CCTAAAGGCC	1950
GAGTGCCT	CTACGTAAAC	GGGGTATTAT	CTCGAACAAAG	TCTGAGATCT	2000
GGCAATTCA	TTAAAGATAT	GCCAGATGTA	ACGCATGTGC	AAATCGGAGC	2050
AACCAAGCGT	GCCAACAATA	CGGTTGGGG	GTCAAATCTA	CAGATTGGAA	2100
ATCTCACTGT	GTATAATCGT	GCTTTAACAC	CAGAAGAGGT	ACAAAAACGT	2150
AGTCAACTTT	TTAAACGCTC	AGATTTAGAA	AAAAAAACTAC	CTGAAGGAGC	2200
GGCTTTAACCA	GAGAAAACGG	ACATATTGCA	AAGCGGGCGT	AACGGTAAAC	2250
CAAATAAAGA	TGGAATCAAG	AGTTATCGTA	TTCCAGCACT	TCTCAAGACA	2300
GATAAAGGAA	CTTTGATCGC	AGGTGCAGAT	GAACGCCGTC	TCCATTGAG	2350
TGACTGGGGT	GATATCGGT	TGGTCATCAG	ACGTAGTGAA	GATAATGGTA	2400
AAACTTGGGG	TGACCGAGTA	ACCATTACCA	ACTTACGTGA	CAATCCAAA	2450
GCTTCTGACC	CATCGATCGG	TTCACCACTG	AATATCGATA	TGGTGGTGGT	2500
TCAAGATCCT	GAAACCAAAC	GAATCTTTTC	TATCTATGAC	ATGTTCCCAG	2550
AAGGGAAGGG	AATCTTTGGA	ATGTCTTCAC	AAAAAGAAGA	AGCCTACAAA	2600
AAAATCGATG	AAAAAACCTA	TCAAATCCTC	TATCGTGAAG	GAGAAAAGGG	2650
AGCTTATACC	ATTGAGAAA	ATGGTACTGT	CTATACACCA	GATGGTAAGG	2700
CGACAGACTA	TCGCGTTGTT	GTAGATCCTG	TTAAACCAGC	CTATAGCGAC	2750
AAGGGGGATC	TATACAAGGG	TAACCAATT	CTAGGCAATA	TCTACTTCAC	2800
AACAAACAAA	ACTTCTCCAT	TTAGAATTGC	CAAGGATAGC	TATCTATGGA	2850
TGTCCTACAG	TGATGACGAC	GGGAAGACAT	GGTCAGCGCC	TCAAGATATT	2900
ACTCCGATGG	TCAAAGCCGA	TTGGATGAAA	TTCTTGGGTG	TAGGTCTGG	2950
AACAGGAATT	GTACTTCGGA	ATGGGCCTCA	CAAGGGACGG	ATTTTGATAC	3000
CGGTTTATAC	GACTAATAAT	GTATCTCACT	TAAATGGCTC	GCAATCTTCT	3050
CGTATCATCT	ATTGAGATGA	TCATGGAAAA	ACTTGGCATG	CTGGAGAAGC	3100
GGTCAACGAT	AACCGTCAGG	TAGACGGTCA	AAAGATCCAC	TCTTCTACGA	3150

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TGAACAATAG	ACGTGCGCAA	AATACAGAAT	CAACGGTGGT	ACAACTAAAC	3200
AATGGAGATG	TTAAACTCTT	TATGCGTGGT	TTGACTGGAG	ATCTTCAGGT	3250
TGCTACAAGT	AAAGACGGAG	GAGTGACTTG	GGAGAAGGAT	ATCAAACGTT	3300
ATCCACACGGT	TAAAGATGTC	TATGTTCAAA	TGTCTGCTAT	CCATACGATG	3350
CACGAAGGAA	AAGAATACAT	CATCCTCAGT	AATGCAGGTG	GACCGAAACG	3400
TGAAAATGGG	ATGGTCCACT	TGGCACGTGT	CGAAGAAAAT	GGTGAGTTGA	3450
CTTGGCTCAA	ACACAATCCA	ATTCAAAAAG	GAGAGTTTGC	CTATAATTG	3500
CTCCAAGAAT	TAGGAAATGG	GGAGTATGGC	ATCTTGTATG	AACATACTGA	3550
AAAAGGACAA	AATGCCTATA	CCCTATCATT	TAGAAAATTT	AATTGGGACT	3600
TTTTGAGCAA	AGATCTGATT	TCTCCTACCG	AAGCGAAAGT	GAAGCGAACT	3650
AGAGAGATGG	GCAAAGGAGT	TATTGGCTTG	GAGTTCGACT	CAGAAGTATT	3700
GGTCAACAAAG	GCTCCAACCC	TTCAATTGGC	AAATGGTAAA	ACAGCACGCT	3750
TCATGACCCA	GTATGATACA	AAAACCCCTCC	TATTTACAGT	GGATTTCAGAG	3800
GATATGGGTC	AAAAAGTTAC	AGGTTTGCA	GAAGGTGCAA	TTGAAAGTAT	3850
GCATAATTAA	CCAGTCTCTG	TGGCGGGCAC	TAAGCTTTCG	AATGGAATGA	3900
ACGGAAAGTGA	AGCTGCTGTT	CATGAAGTGC	CAGAATACAC	AGGCCCATTA	3950
GGGACATCCG	GCGAAGAGCC	AGCTCCAACA	GTCGAGAACG	CAGAATACAC	4000
AGGCCCACTA	GGGACATCCG	GCGAAGAGCC	AGCCCCGACA	GTCGAGAACG	4050
CAGAATACAC	AGGCCCACTA	GGGACAGCTG	GTGAAGAACG	AGCTCCAACA	4100
GTCGAGAACG	CAGAATTTCAC	AGGGGGAGTT	AATGGTACAG	AGCCAGCTGT	4150
TCATGAAATC	GCAGAGTATA	AGGGATCTGA	TTCGCTTGT	ACTCTTACTA	4200
CAAAAGAAGA	TTATACCTAC	AAAGCTCCTC	TTGCTCAGCA	GGCACTTCCT	4250
GAAACAGGAA	ACAAGGAGAG	TGACCTCCTA	GCTTCACTAG	GACTAACAGC	4300
TTTCTTCCTT	GGTCTGTTA	CGCTAGGGAA	AAAGAGAGAA	CAATAAGAGA	4350
AGAATTCTAA	ACATTGATT	TTGTAAAAAT	AGAAGGGAGAT	AGCAGGTTTT	4400
CAAGCCTGCT	ATCTTTTTT	GATGACATTC	AGGCTGATAC	GAAATCATAA	4450
GAGGTCTGAA	ACTACTTCA	GAGTAGTCTG	TTCTATAAAA	TATAGTAGAT	4500

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36
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GATCCAAGCT	TATCGATATC	ATCAAAAAGT	TGGCGAACCT	TTTCAAATTT	50
TGGTTCAAAT	TCTTGAGATG	TATAGAATTC	AAAATATTTA	CCATTGCGAT	100
AGTCTGATTG	CTCAAAGTCT	TGATACTTTT	CTCCACGCTC	TTTTGCAATT	150
TCCATTGAAC	GTTCGATGGA	ATAATAGTTC	ATAATCATAA	AGAATATATT	200
AGCAAAGTCT	TTTGCTTCTT	CAGATTCATATA	GCCAATTTA	TTTTTAGCTA	250
GATAACCATG	TAAGTTCATT	ACTCCTAGTC	CAACAGAATG	TAGTTCACTA	300
TTCGCTTTT	TTACACCTGG	TGCATTTGA	ATATTTGCTT	CATCACTTAC	350
AACTGTAAGA	GCATCCATAC	CTGTGAACAC	AGAATCTCTG	AATTACCTG	400
ATTCCATAAC	ATTCACTATA	TTCAATGAGC	CTAAGTTACA	TGAAATATCT	450
CTTTTAATTT	CATCTTCAAT	TCCATAGTCG	TTAATTACTG	ATGTCTCTG	500
TAATTGGAAA	ATTTCACTAC	ATAAATTACT	CATTTTAATT	TGCCCAATAT	550
TTGAATTCGC	ATGTACTTTG	TTTGCATTAT	CTTTAAACAT	AAGATATGGA	600
TAACCAGACT	GTAATTGTGT	TTGTGCAATC	ATATTTAACCA	TTTCACGTGC	650
GTCTTTTTTC	TTTTTATCGA	TTTCGAACCC	GGGGTACCGA	ATTCCCTCGAG	700
	TCTAG				705

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(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GATCAATCTT	TGTCGGTACA	CGATATTCTT	CACGACTAAA	TAAACGCTCA	50
TTCGCGATTT	TATAAATGAA	TGTTGATAAC	AATGTTGTAT	TATCTACTGA	100
AATCTCATTA	CGTTGCATCG	GAAACATTGT	GTTCTGTATG	TAAAAGCCGT	150
CTTGATAATC	TTTAGTAGTA	CCGAAGCTGG	TCATACGAGA	GTTATATTTT	200
CCAGCCAAAA	CGATATTTTT	ATAATCATTA	CGTGAAAAAG	GTTTCCCTTC	250
ATTATCACAC	AAATATTTTA	GCTTTCACT	TTCTATATCA	ACTGTAGCTT	300
CTTTATCCAT	ACGTTGAATA	ATTGTACGAT	TCTGACGCAC	CATCTTTGTC	350
ACACCTTAA	TGTTATTTGT	TTTAAAAGCA	TGAATAAGTT	TTTCAACACA	400
ACGATGTGAA	TCTTCTAAGA	AGTCACCGTA	AAATGAAGGA	TC	442

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Enterococcus faecalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GCAATACAGG GAAAAATGTC

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(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Enterococcus faecalis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTTCATCAAA CAATTAAC

20

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Enterococcus faecalis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

GAACAGAAGA AGCCAAAAAA

20

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Enterococcus faecalis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GCAATCCCAA ATAATACGGT

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(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
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- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

GCTTTCCAGC GTCATATTG

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(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GATCTCGACA AAATGGTGA

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(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

CACCCGCTTG CGTGGCAAGC TGCCC

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(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CGTTTGTGGA TTCCAGTTCC ATCCG

25

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

TCACCCGCTT GCGTGGC

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(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGAACCTGGAA TCCACAAAC

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(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases

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- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

TGAAGCACTG GCCGAAATGC TGCCT

25

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GATGTACAGG ATTCGTTGAA GGCTT

25

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

TAGCGAAGGC GTAGCAGAAA CTAAC

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(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

GCAACCCGAA CTCAACGCCG GATTT

25

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

ATACACAAAGG GTCGCATCTG CGGCC

25

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

TGGGTATGCA TTGCAGACCT TGTGGC

26

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases

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- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GCTTTCACTG GATATCGCGC TTGGG

25

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GCAACCCGAA CTCAACGCC

19

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

GCAGATGCGA CCCTTGTGT

19

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(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Klebsiella pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GTGGTGTGCGT TCAGCGCTTT CAC

23

(2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Klebsiella pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GCGATATTCA CACCCCTACGC AGCCA

25

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Klebsiella pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GTCGAAAATG CCGGAAGAGG TATACG

26

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid

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(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

ACTGAGCTGC AGACCGGTAA AACTCA

26

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GACAGTCAGT TCGTCAGCC

19

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

CGTAGGGTGT GAATATCGC

19

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(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

CGTGATGGAT ATTCTTAACG AAGGGC

26

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

ACCAAACTGT TGAGCCGCCT GGA

23

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GTGATCGCCC CTCATCTGCT ACT

23

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases

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- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

CGCCCTTCGT TAAGAATATC CATCAC

26

(2) INFORMATION FOR SEQ ID NO: 67:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TCGCCCTCA TCTGCTACT

19

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

GATCGTGATG GATATTCTT

19

109

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CAGGAAGATG CTGCACCGGT TGTG

25

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

TGGTTCACTG ACTTTGCGAT GTTTC

25

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

TCGAGGATGG CATGCACTAG AAAAT

25

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid

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(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

CGCTGATTAG GTTTCGCTAA AATCTTATTA

30

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TTGATCCTCA TTTTATTAAT CACATGACCA

30

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

GAAACATCGC AAAGTCAGT

19

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(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Proteus mirabilis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

ATAAAATGAG GATCAAGTTC

20

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Proteus mirabilis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CCGCCTTTAG CATTAAATTGG TGTTTATAGT

30

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Proteus mirabilis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

CCTATTGCAG ATACCTTAAA TGTCTTGGGC

30

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid

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- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

AGTAAAATGA AATAAGAACAA GGACAG

26

- (2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

AAAACAGGAT AGGAGAACCGG GAAAA

25

- (2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Proteus mirabilis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

TTGAGTGATG ATTCACTGA CTCCC

25

- (2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

GTCAGACAGT GATGCTGACG ACACA

25

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Proteus mirabilis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

TGGTTGTCAT GCTGTTGTG TGAAAAT

27

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CGAGCGGGTG GTGTTCATC

19

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(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Pseudomonas aeruginosa*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

19

CAAGTCGTCG TCGGAGGG

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Pseudomonas aeruginosa*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

19

TCGCTGTTCA TCAAGACCC

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Pseudomonas aeruginosa*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

19

CCGAGAACCA GACTTCATC

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid

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(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

AATGCCGGCTG TACCTCGGCG CTGGT

25

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

GGCGGAGGGC CAGTTGCACC TGCCA

25

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

AGCCCCTGCTC CTCGGCAGCC TCTGC

25

116

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

TGGCTTTGCAACCGCGTTCAGGTT

25

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

GCGCCCGCGA GGGCATGCTT CGATG

25

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

ACCTGGCGC CAACTACAAG TTCTA

25

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid

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- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GGCTACGCTG CCGGGCTGCA GGCG

25

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

CCGATCTACA CCATCGAGAT GGGCG

25

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Pseudomonas aeruginosa*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

GAGCGCGGCT ATGTGTTCGT CGGCT

25

118

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CGTTTTTACC CTTACCTTTT CGTACTACC

29

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

TCAGGCAGAG GTAGTACGAA AAGGTAAGGG

30

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CGTTTTTACC CTTACCTTTT CGTACT

26

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: Nucleic acid

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(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

ATCGATCATC ACATTCCATT TGTTTTTA

28

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

CACCAAGTTT GACACGTGAA GATTCA

27

(2) INFORMATION FOR SEQ ID NO: 101

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus saprophyticus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

ATGAGTGAAG CGGAGTCAGA TTATGTGCAG

30

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(2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Staphylococcus saprophyticus*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

CGCTCATTAC GTACAGTGAC AATCG

25

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Staphylococcus saprophyticus*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CTGGTTAGCT TGACTCTTAA CAATCTTGTC

30

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Staphylococcus saprophyticus*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

GACGCGATTG TCACTGTACG TAATGAGCGA

30

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 bases
 - (B) TYPE: Nucleic acid

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(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GCGTCAGAAA AAGTAGGCGA AATGAAAG

28

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

AGCGGCTCTA TCTTGTAATG ACACA

25

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GAAACGTGAA CTCCCCCTCTA TATAA

25

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(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

GCCCCAAAAC AATGAAACAT ATGGT

25

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CTGCAGATT TGGAATCATA TCGCC

25

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

TGGTTTGACC AGTATTTAAC GCCAT

25

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid

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- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CAACGGCACC TGATGTACCT TGTAC

25

(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

GGCACCTGAT GTACCTTG

18

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

AACAGCTCAC ACGCATT

17

124

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

TTACAACCTG CACCACAAAGT CATCA

25

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GTACAAACAA GCCGTCAGCG ACTTA

25

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

CAATCTGGGT GTGTGCGTTC ACT

23

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid

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- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

GCTACTTTGT CAGCTTTAGC CATTCA

26

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

TGTTTTGAGC TTTTTATTTT TTGA

24

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

CGCTGACGGC TTGTTTGTAC CA

22

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(2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

TCTGTGCTAG AGACTGCCCC ATTTC

25

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

CGATGTCTTG ATTGAGCAGG GTTAT

25

(2) INFORMATION FOR SEQ ID NO: 122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

ATCCCCACCTT AGGCGGGCTGG CTCCA

25

127

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

ACGTCAAGTC ATCATGGCCC TTACGAGTAG G

31

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

GTGTGACGGG CGGTGTGTAC AAGGC

25

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GAGTTGCAGA CTCCAATCCG GACTACGA

28

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

GGAGGAAGGT GGGGATGACG

20

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(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

ATGGTGTGAC GGGCGGTGTG

20

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CCCTATACAT CACCTTGCAG TTTAGCAGAG AG

32

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

GGGGGGACCA TCCTCCAAGG CTAAATAC

28

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(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

CGTCCACTTT CGTGTTTGCA GAGTGCTGTG TT

32

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

CAGGAGTACG GTGATTTTA

20

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

ATTTCTGGTT TGGTCATACA

20

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(2) INFORMATION FOR SEQ ID NO: 133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Proteus mirabilis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CGGGAGTCAG TGAAATCATC

20

(2) INFORMATION FOR SEQ ID NO: 134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Proteus mirabilis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

CTAAAATCGC CACACCTCTT

20

(2) INFORMATION FOR SEQ ID NO: 135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Klebsiella pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

GCAGCGTGGT GTCGTTCA

18

(2) INFORMATION FOR SEQ ID NO: 136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid

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- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

AGCTGGCAAC GGCTGGTC

18

(2) INFORMATION FOR SEQ ID NO: 137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

ATTCACACCC TACGCAGCCA

20

(2) INFORMATION FOR SEQ ID NO: 138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

ATCCGGCAGC ATCTCTTTGT

20

1321

(2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Staphylococcus saprophyticus*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

CTGGTTAGCT TGACTCTTAA CAATC

25

(2) INFORMATION FOR SEQ ID NO: 140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Staphylococcus saprophyticus*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

TCTTAACGAT AGAATGGAGC AACTG

25

(2) INFORMATION FOR SEQ ID NO: 141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pyogenes*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TGAAAATTCT TGTAACAGGC

20

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid

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- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

GGCCACCAAGC TTGCCCAATA

20

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

ATATTTCTT TATGAGGGTG

20

(2) INFORMATION FOR SEQ ID NO: 144:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pyogenes*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

ATCCTTAAAT AAAGTTGCCA

20

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(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

ATCAAAAAGT TGGCGAACCT TTTCA

25

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

CAAAAGAGCG TGGAGAAAAG TATCA

25

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

TCTCTTTAATTTCATCTTC AATTCCATAG

30

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid

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(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus epidermidis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

AAACACAATT ACAGTCTGGT TATCCATATC

30

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

CTTCATTTA CGGTGACTTC TTAGAAGATT

30

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

TCAACTGTAG CTTCTTTATC CATACTTGA

30

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(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

ATATTTAGC TTTTCAGTTT CTATATCAAC

30

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

AATCTTGTC GGTACACGAT ATTCTTCACG

30

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

CGTAATGAGA TTTCACTAGA TAATACAACA

30

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid

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- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

TTTAACGATC CTTTTACTCC TTTTG

25

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Haemophilus influenzae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

ACTGCTGTTG TAAAGAGGTT AAAAT

25

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

ATTTGGTGAC GGGTGACTTT

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(2) INFORMATION FOR SEQ ID NO: 157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

GCTGAGGATT TGTCTTCTT

20

(2) INFORMATION FOR SEQ ID NO: 158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

GAGCGGTTTC TATGATTGTA

20

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

ATCTTTCCTT TCTTGTTCTT

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid

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(C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moraxella catarrhalis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

GCTCAAATCA GGGTCAGC

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(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 861 base pairs
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

ATGAGTATTTC	AACATTTCCG	TGTCGCCCTT	ATTCCCTTTT	TTGCGGCATT	50
TTGCCTTCCT	GTTTTGCTC	ACCCAGAAAC	GCTGGTAAAA	GTAAAAGATG	100
CTGAAGATCA	GTTGGGTGCA	CGAGTGGGTT	ACATCGAACT	GGATCTCAAC	150
AGCGGTAAGA	TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGAT	200
GAGCACTTTT	AAAGTTCTGC	TATGTGGCGC	GGTATTATCC	CGTGTGACCG	250
CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	ACTATTCTCA	GAATGACTTG	300
GTTGAGTACT	CACCAAGTCAC	AGAAAAGCAT	CTTACGGATG	GCATGACAGT	350
AAGAGAATTAA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	400
ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTG	450
CACAACATGG	GGGATCATGT	AACTCGCCTT	GATCGTTGGG	AACCGGAGCT	500
GAATGAAGCC	ATACCAAACG	ACGAGCGTGA	CACCACGATG	CCTGCAGCAA	550
TGCCAACAAAC	GTTGCGCAAA	CTATTAAC TG	GGAACTACT	TACTCTAGCT	600
TCCC GGCAAC	AATTAATAGA	CTGGATGGAG	GGGGATAAAG	TTGCAGGACC	650
ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GT TTATTGCT	GATAAATCTG	700
GAGCCGGTGA	GGGTGGGTCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	750
GGTAAGCCCT	CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	800
TATGGATGAA	CGAAATAGAC	AGATCGCTGA	GATAGGTGCC	TCACTGATTA	850
AGCATTGGTA	A				861

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 918 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

ATGTTAAATA	AGTTAAAAAT	CGGCACATTA	TTATTGCTGA	CATTAACGGC	50
TTGTCGCC	AATTCTGTT	ATTCGTAAC	GTCTAATCCG	CAGCCTGCTA	100
GTGCGCCTGT	GCAACAATCA	GCCACACAAG	CCACCTTTCA	ACAGACTTTG	150
GCGAATTG	AACAGCAGTA	TCAAGCCGA	ATTGGCGTTT	ATGTATGGGA	200
TACAGAAACG	GGACATTCTT	TGTCTTATCG	TGCAGATGAA	CGCTTGCTT	250
ATGCGTCCAC	TTTCAAGGCG	TTGTTGGCTG	GGGCGGTGTT	GCAATCGCTG	300
CCTGAAAAAG	ATTTAAATCG	TACCATTTCA	TATAGCCAAA	AAGATTTGGT	350
TAGTTATTCT	CCCGAAACCC	AAAAATACGT	TGGCAAAGGC	ATGACGATTG	400
CCCAATTATG	TGAAGCAGCC	GTGCGGTTA	GCGACAAACAG	CGCGACCAAT	450
TTGCTGCTA	AAGAATTGGG	TGGCGTGGAA	CAATATCAAC	GTATTTGCG	500
ACAATTAGGC	GATAACGTAA	CCCATACCAA	TCGGCTAGAA	CCCGATTTAA	550
ATCAAGCCAA	ACCCAACGAT	ATTCGTGATA	CGAGTACACC	CAAACAAATG	600
GCGATGAATT	TAAATGCGTA	TTTATTGGC	AACACATTAA	CCGAATCGCA	650
AAAAACGATT	TTGTGGAATT	GGTTGGACAA	TAACGCAACA	GGCAATCCAT	700
TGATTGCGC	TGCTACGCCA	ACATCGTGG	AAAGTGTACGA	TAAAAGCGGG	750
GCAGGTAAAT	ATGGTGTACG	CAATGATATT	GCAGGTGGTTC	GCATACCAAA	800
TCGAAACCG	ATTGTGATGG	CAATCATGAG	TACGCAATT	ACCGAAGAAG	850
CCAAATTCAA	CAATAAATTA	GTAGAAGATG	CAGCAAAGCA	AGTATTCAT	900
ACTTACAGC	TCAACTAA				918

(2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 864 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

ATGCGTTATA	TTCGCCTGTG	TATTATCTCC	CTGTTAGCCA	CCCTGCCGCT	50
GGCGGTACAC	GCCAGCCCGC	AGCCGCTTGA	GCAAATTAAA	CTAAGCGAAA	100
GCCAGCTGTC	GGGCCGCGTA	GGCATGATAG	AAATGGATCT	GGCCAGCGGC	150

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CGCACGCTGA	CCGCCTGGCG	CGCCGATGAA	CGCTTTCCCA	TGATGAGCAC	200
CTTTAAAGTA	GTGCTCTGCG	GCGCAGTGCT	GGCGCGGGTG	GATGCCGGTG	250
ACGAACAGCT	GGAGCGAAAG	ATCCACTATC	GCCAGCAGGA	TCTGGTGGAC	300
TACTCGCCGG	TCAGCGAAAA	ACACCTTGCC	GACGCAATGA	CGGTCGGCGA	350
ACTCTGCGCC	GCCGCCATTA	CCATGAGCGA	TAACAGCGCC	GCCAATCTGC	400
TACTGGCCAC	CGTCGGCGGC	CCCGCAGGAT	TGACTGCCTT	TTTGCGCCAG	450
ATCGGCGACA	ACGTCACCCG	CCTTGACCGC	TGGGAAACGG	AACTGAATGA	500
GGCGCTTCCC	GGCGACGCC	GCGACACCAC	TACCCCGGCC	AGCATGGCCG	550
CGACCCCTGCG	CAACGTTGGC	CTGACCAGCC	ACCGTCTGAG	CGCCC GTTCG	600
CAACGGCAGC	TGCTGCAGTG	GATGGTGGAC	GATCGGGTCG	CCGGACCGTT	650
GATCCGCTCC	GTGCTGCCGG	CGGGCTGGTT	TATGCCGAT	AAGACCGGAG	700
CTGGCGAGCG	GGGTGCGCGC	GGGATTGTCG	CCCTGCTTGG	CCCGAATAAC	750
AAAGCAGAGC	GCATTGTGGT	GATTTATCTG	CGGGATAACCC	CGGGAGCAT	800
GGCCGAGCGA	AATCAGCAA	TCGCCGGAT	CGGCAAGGCG	CTGTACGAGC	850
ACTGGCAACG	CTAA				864

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

ATGGACACAA	CGCAGGTCAC	ATTGATACAC	AAAATTCTAG	CTGCGGCAGA	50
TGAGCGAAAT	CTGCCGCTCT	GGATCGGTGG	GGGCTGGCG	ATCGATGCAC	100
GGCTAGGGCG	TGTAACACGC	AAGCACGATG	ATATTGATCT	GACGTTTCCC	150
GGCGAGAGGC	GCGGCGAGCT	CGAGGCAATA	GTTGAAATGC	TCGGCGGGCG	200
CGTCATGGAG	GAGTTGGACT	ATGGATTCTT	ACCGGAGATC	GGGGATGAGT	250
TACTTGACTG	CGAACCTGCT	TGGTGGGCAG	ACGAAGCGTA	TGAAATCGCG	300
GAGGCTCCGC	AGGGCTCGTG	CCCAGAGGCG	GCTGAGGGCG	TCATCGCCGG	350
GCGGCCAGTC	CGTTGTAACA	GCTGGGAGGC	GATCATCTGG	GATTACTTTT	400
ACTATGCCGA	TGAAGTACCA	CCAGTGGACT	GGCCTACAAA	GCACATAGAG	450
TCCTACAGGC	TCGCATGCAC	CTCACTCGGG	GCGGAAAAGG	TTGAGGTCTT	500
GCGTGCCGCT	TTCAGGTGCG	GATATGCGGC	CTAA		534

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 465 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

ATGGGCATCA	TTCGCACATG	TAGGCTCGGC	CCTGACCAAG	TCAAATCCAT	50
GCGGGCTGCT	CTTGATCTTT	TCGGTCGTGA	GTTCCGGAGAC	GTAGCCACCT	100
ACTCCCAACA	TCAGCCGGAC	TCCGATTACC	TCGGGAACCTT	GCTCCGTAGT	150
AAGACATTCA	TCGCGCTTGC	TGCCCTCGAC	CAAGAAGCGG	TTGTTGGCGC	200
TCTCGCGGCT	TACGTTCTGC	CCAGGTTTGA	GCAGCCGCGT	AGTGAGATCT	250
ATATCTATGA	TCTCGCAGTC	TCCGGCGAGC	ACCGGAGGCA	GGGCATTGCC	300
ACCGCGCTCA	TCAATCTCCT	CAAGCATGAG	GCCAACGCGC	TTGGTGCTTA	350
TGTGATCTAC	GTGCAAGCAG	ATTACGGTGA	CGATCCCGCA	GTGGCTCTCT	400
ATACAAAAGTT	GGGCATACGG	GAAGAAGTGA	TGCACTTTGA	TATCGACCCA	450
AGTACCGCCA	CCTAA				465

(2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 861 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

ATGCATACGC	GGAAGGCAAT	AACGGAGGCG	CTTCAAAAAC	TCGGAGTCCA	50
AACCGGTGAC	CTATTGATGG	TGCATGCCTC	ACTTAAAGCG	ATTGGTCCGG	100
TCGAAGGAGG	AGCGGAGACG	GTCGTTGCCG	CGTTACGCTC	CGCGGTTGGG	150
CCGACTGGCA	CTGTGATGGG	ATACGCATCG	TGGGACCGAT	CACCCCTACGA	200
GGAGACTCGT	AATGGCGCTC	GGTTGGATGA	CAAAACCGC	CGTACCTGGC	250
CGCCGTTCGA	TCCCGCAACG	GCCGGGACTT	ACCGTGGTT	CGGCCTGCTG	300
AATCAGTTTC	TGGTTCAAGC	CCCCGGCGCG	CGGCGCAGCG	CGCACCCGA	350
TGCATCGATG	GTCGCGGTTG	GTCCACTGGC	TGAAAACGCTG	ACGGAGCCTC	400
ACAAGCTCGG	TCACGCTTG	GGGGAAGGGT	CGCCCGTCGA	GCGGTTCGTT	450
CGCCTTGGCG	GGAAAGGCCCT	GCTGTTGGGT	GCGCCGCTAA	ACTCCGTTAC	500
CGCATTGCAC	TACGCCGAGG	CGGTTGCCGA	TATCCCCAAC	AAACGGCGGG	550
TGACGTATGA	GATGCCGATG	CTTGGAAAGCA	ACGGCGAAGT	CGCCTGGAAA	600

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ACGGCATCGG	ATTACGATT	AAACGGCATT	CTCGATTGCT	TTGCTATCGA	650
AGGAAAGCCG	GATGCGGTCG	AAACTATAGC	AAATGCTTAC	GTGAAGCTCG	700
GTCGCCATCG	AGAAGGTGTC	GTGGGCTTTG	CTCAGTGCTA	CCTGTTGAC	750
GCGCAGGACA	TCGTGACGTT	CGGCGTCACC	TATCTTGAGA	AGCATTTCGG	800
AACCACTCCG	ATCGTGCCAG	CACACGAAGT	CGCCGAGTGC	TCTTGCGAGC	850
CTTCAGGTTA	G				861

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 816 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

ATGACCGATT	TGAATATCCC	GCATACACAC	GCGCACCTTG	TAGACGCATT	50
TCAGGCGCTC	GGCATCCGCG	CGGGGCAGGC	GCTCATGCTG	CACGCATCCG	100
TTAAAGCAGT	GGGCGCGGTG	ATGGGCGGCC	CCAATGTGAT	CTTGCAGGCG	150
CTCATGGATG	CGCTCACGCC	CGACGGCACG	CTGATGATGT	ATGCGGGATG	200
GCAAGACATC	CCCGACTTTA	TCGACTCGCT	GCCGGACGCG	CTCAAGGCCG	250
TGTATCTTGA	GCAGCACCCA	CCCTTTGACC	CCGCCACCGC	CCGCGCCGTG	300
CGCGAAAACA	GCGTGCTAGC	GGAATTTTG	CGCACATGGC	CGTGCCTGCA	350
TCGCAGCGCA	AACCCCGAAG	CCTCTATGGT	GGCGGTAGGC	AGGCAGGCCG	400
CTTTGCTGAC	CGCTAACAC	CGCCTGGATT	ATGGCTACGG	AGTCGAGTCG	450
CCGCTGGCTA	AACTGGTGGC	AATAGAAGGA	TACGTGCTGA	TGCTTGGCGC	500
GCCGCTGGAT	ACCATCACAC	TGCTGCACCA	CGCGGAATAT	CTGGCCAAGA	550
TGCGCCACAA	GAACGTGGTC	CGCTACCCGT	GCCCGATTCT	GCGGGACGGG	600
CGCAAAGTGT	GGGTGACCGT	TGAGGACTAT	GACACCGGTG	ATCCGCACGA	650
CGATTATAGT	TTTGAGCAAA	TCGCGCGCGA	TTATGTGGCG	CAGGGCGGCCG	700
GCACACGCGG	CAAAGTCGGT	GATGCGGATG	CTTACCTGTT	CGCCGCGCAG	750
GACCTCACAC	GGTTTGGGGT	GCAGTGGCTT	GAATCACGGT	TCGGTGACTC	800
AGCGTCATAC	GGATAG				816

(2) INFORMATION FOR SEQ ID NO: 168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

ATGCTCTATG	AGTGGCTAAA	TCGATCTCAT	ATCGTCGAGT	GGTGGGGCGG	50
AGAAGAAGCA	CGCCCGACAC	TTGCTGACGT	ACAGGAACAG	TACTTGCCAA	100
GCGTTTTAGC	GCAAGAGTCC	GTCACTCCAT	ACATTGCAAT	GCTGAATGGA	150
GAGCCGATTG	GGTATGCCA	GTCGTACGTT	GCTCTTGAA	GCGGGGACGG	200
ATGGTGGGAA	GAAGAAACCG	ATCCAGGAGT	ACGCGGAATA	GACCAGTTAC	250
TGGCGAATGC	ATCACAACTG	GGCAAAGGCT	TGGGAACCAA	GCTGGTTCGA	300
GCTCTGGTTG	AGTTGCTGTT	CAATGATCCC	GAGGTACCCA	AGATCCAAAC	350
GGACCCGTCG	CCGAGCAACT	TGCGAGCGAT	CCGATGCTAC	GAGAAAGCGG	400
GGTTTGAGAG	GCAAGGTACC	GTAACCACCC	CAGATGGTCC	AGCCGTGTAC	450
ATGGTTCAAA	CACGCCAGGC	ATTCGAGCGA	ACACCGCAGTG	ATGCCTAA	498

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2007 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

ATGAAAAAAGA	AAAAAATTGT	TCCACTTATT	TTAATAGTTG	TAGTTGTCGG	50
TTTTGGTATA	TATTTTTATG	CTTCAAAAGA	AAAAGAAATT	AATAATACTA	100
TTGATGCAAT	TGAAGATAAA	AATTTCAAAC	AAGTTTATAA	AGATAGCAGT	150
TATATTCTA	AAAGCGATAA	TGGTGAAGTA	AAAATGACTG	AACGTCCGAT	200
AAAAATATAT	AATAGTTTAG	GGCTTAAAGA	TATAAACATT	CAGGATCGTA	250
AAATAAAAAA	AGTATCTAAA	AATAAAAAAC	GAGTAGATGC	TCAATATAAA	300
ATTAACACAA	ACTACGGTAA	CATTGATCGC	AACGTTCAAT	TTAATTGT	350
TAAAGAAGAT	GGTATGTGGA	AGTTAGATTG	GGATCATAGC	GTCATTATTC	400
CAGGAATGCA	GAAAGACCAA	AGCATAACATA	TTGAAAATT	AAAATCAGAA	450
CGTGGTAAAA	TTTTAGACCG	AAACAATGTG	GAATTGGCCA	ATACAGGAAC	500
ACATATGAGA	TTAGGCATCG	TTCCAAAGAA	TGTATCTAAA	AAAGATTATA	550
AAGCAATCGC	TAAAGAACTA	AGTATTTCTG	AAGACTATAT	CAACAAACAA	600
TGGATCAAAA	TTGGGTACAA	GATGATACCT	TCGTTCCACT	TTAAAACCGT	650
TAAAAAAATG	GATGAATATT	TAAGTGATTT	CGCAAAAAAA	TTTCATCTTA	700
CAACTAATGA	AACAGAAAAGT	CGTAACTATC	CTCTAGAAAA	AGCGACTTCA	750
CATCTATTAG	GTTATGTG	TCCCATTAAC	TCTGAAGAAT	AAAAACAAAA	800

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AGAATATAAA	GGCTATAAAAG	ATGATGCA GT	TATTGGTAAA	AAGGGACTCG	850
AAAAACTTTA	CGATAAAAAG	CTCCAACATG	AAGATGGCTA	TCGTGTCACA	900
ATCGTTGACG	ATAATAGCAA	TACAATCGCA	CATACATTAA	TAGAGAAAAA	950
GAAAAAAAGAT	GGCAAAGATA	TTCAACTAAC	TATTGATGCT	AAAGTTCAAA	1000
AGAGTATTAA	TAACAAACATG	AAAAATGATT	ATGGCTCAGG	TACTGCTATC	1050
CACCCCTCAAA	CAGGTGAATT	ATTAGCACTT	GTAAGCACAC	CTTCATATGA	1100
CGTCTATCCA	TTTATGTATG	GCATGAGTAA	CGAAGAAATAT	AATAAATTAA	1150
CCGAAGATAA	AAAAGAACCT	CTGCTCAACA	AGTTCAGAT	TACAACTTCA	1200
CCAGGTTCAA	CTCAAAAAAT	ATTAACAGCA	ATGATTGGGT	TAATAACAA	1250
AACATTAGAC	GATAAAACAA	GTTATAAAAT	CGATGGTAAA	GGTTGGCAAA	1300
AAGATAAAATC	TTGGGGTGGT	TACAACGTTA	CAAGATATGA	AGTGGTAAAT	1350
GGTAATATCG	ACTTAAAACA	AGCAATAGAA	TCATCAGATA	ACATTTCTT	1400
TGCTAGAGTA	GCACTCGAAT	TAGGCAGTAA	GAAATTGAA	AAAGGCATGA	1450
AAAAACTAGG	TGTTGGTGAA	GATATACCAA	GTGATTATCC	ATTTTATAAT	1500
GCTCAAATTT	CAAACAAAAA	TTTAGATAAT	GAAATATTAT	TAGCTGATT	1550
AGGTACCGA	CAAGGTGAAA	TACTGATTAA	CCCAGTACAG	ATCCTTCAA	1600
TCTATAGCGC	ATTAGAAAAT	AATGGCAATA	TTAACGCACC	TCACTTATTA	1650
AAAGACACGA	AAAACAAAGT	TTGGAAGAAA	AAATTATT	CCAAAGAAAA	1700
TATCAATCTA	TTAAATGATG	GTATGCAACA	AGTCGTAAAT	AAAACACATA	1750
AAGAAGATAT	TTATAGATCT	TATGCAAAC	TAATTGGCAA	ATCCGGTACT	1800
GCAGAACTCA	AAATGAAACA	AGGAGAAAGT	GGCAGACAAA	TTGGGTGGTT	1850
TATATCATAT	GATAAAAGATA	ATCCAAACAT	GATGATGGCT	ATTAATGTTA	1900
AAGATGTACA	AGATAAAAGGA	ATGGCTAGCT	ACAATGCCAA	AATCTCAGGT	1950
AAAGTGTATG	ATGAGCTATA	TGAGAACGGT	AATAAAAAT	ACGATATAGA	2000
TGAATAA					2007

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2607 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

ATGAATAACA	TCGGCATTAC	TGTTTATGGA	TGTGAGCAGG	ATGAGGCAGA	50
TGCATTCCAT	GCTCTTCGC	CTCGCTTGG	CGTTATGGCA	ACGATAATTA	100
ACGCCAACGT	GTCGGAATCC	AACGCCAAT	CCGCGCCTT	CAATCAATGT	150
ATCAGTGTGG	GACATAAATC	AGAGATTC	CCCTATTC	TTTTGCGCT	200

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GAAGAGAGCC	GGTGTGAAAT	ATATTTCTAC	CCGAAGCATC	GGCTGCAATC	250
ATATAGATAC	AACTGCTGCT	AAGAGAATGG	GCATCACTGT	CGACAATGTG	300
GCGTACTCGC	CGGATAGCGT	TGCCGATTAT	ACTATGATGC	TAATTCTTAT	350
GGCAGTACGC	AACGTAAAAT	CGATTGTGCG	CTCTGTGGAA	AAACATGATT	400
TCAGGTTGGA	CAGCGACCGT	GGCAAGGTAC	TCAGCGACAT	GACAGTTGGT	450
GTGGTGGAA	CGGGCCAGAT	AGGCAAAGCG	GTTATTGAGC	GGCTGCGAGG	500
ATTTGGATGT	AAAGTGTGG	CTTATAGTCG	CAGCCGAAGT	ATAGAGGTAA	550
ACTATGTACC	GTTTGATGAG	TTGCTGAAA	ATAGCGATAT	CGTTACGCTT	600
CATGTGCCGC	TCAATACGGA	TACGCACTAT	ATTATCAGCC	ACGAACAAAT	650
ACAGAGAATG	AAGCAAGGAG	CATTTCTTAT	CAATACTGGG	CGCGGTCCAC	700
TTGTAGATAC	CTATGAGTTG	GTTAAAGCAT	TAGAAAACGG	GAAACTGGC	750
GGTGCCGCAT	TGGATGTATT	GGAAGGAGAG	GAAGAGTTTT	TCTACTCTGA	800
TTGCACCCAA	AAACCAATTG	ATAATCAATT	TTTACTTAAA	CTTCAAAGAA	850
TGCCTAACGT	GATAATCACA	CCGCATACGG	CCTATTATAC	CGAGCAAGCG	900
TTGCGTGATA	CCGTTGAAAA	AACCATTAAA	AACTGTTTGG	ATTTTGAAG	950
GAGACAGGAG	CATGAATAGA	ATAAAAGTTG	CAATACTGTT	TGGGGGTTGC	1000
TCAGAGGAGC	ATGACGTATC	GGTAAAATCT	GCAATAGAGA	TAGCCGCTAA	1050
CATTAATAAA	AAAAAATACG	AGCCGTTATA	CATTGGAATT	ACGAAATCTG	1100
GTGTATGGAA	AATGTGCGAA	AAACCTTGC	CGGAATGGGA	AAACGACAAT	1150
TGCTATTCAG	CTGTACTCTC	GCCGGATAAA	AAAATGCACG	GATTACTTGT	1200
TAAAAAGAAC	CATGAATATG	AAATCAACCA	TGTTGATGTA	GCATTTTCAG	1250
CTTTGCATGG	CAAGTCAGGT	GAAGATGGAT	CCATACAAGG	TCTGTTGAA	1300
TTGTECGGTA	TCCCTTTGT	AGGCTGGAT	ATTCAAAGCT	CAGCAATTG	1350
TATGGACAAA	TCGTTGACAT	ACATCGTTGC	AAAAATGCT	GGGATAGCTA	1400
CTCCCGCCTT	TTGGGTTATT	AATAAAGATG	ATAGGCCGGT	GGCAGCTACG	1450
TTTACCTATC	CTGTTTTGT	TAAGCCGGCG	CGTTCAAGGCT	CATCCTTCGG	1500
TGTAAAAAAA	GTCAATAGCG	CGGACGAATT	GGACTACGCA	ATTGAATCGG	1550
CAAGACAATA	TGACAGCAA	ATCTTAATTG	AGCAGGCTGT	TTCGGGCTGT	1600
GAGGTCGGTT	GTGCGGTATT	GGGAAACAGT	GCCCGTGTAG	TTGTTGGCGA	1650
GGTGGACCAA	ATCAGGCTGC	AGTACGGAAT	CTTTCTGTATT	CATCAGGAAG	1700
TCGAGCCGGA	AAAAGGCTCT	AAAAACGCAG	TTATAACCCT	TCCCGCAGAC	1750
CTTCAGCAG	AGGAGCGAGG	ACGGATACAG	GAAACGGCAA	AAAAAATATA	1800
TAAAGCGCTC	GGCTGTAGAG	GTCTAGCCCG	TGTGGATATG	TTTTTACAAG	1850
ATAACGGCCG	CATTGTACTG	AACGAAGTCA	ATACTCTGCC	CGGTTTCACG	1900
TCATACAGTC	GTTATCCCCG	TATGATGGCC	GCTGCAGGTA	TTGCACTTCC	1950
CGAACTGATT	GACCGCTTGA	TCGTATTAGC	GTAAAGGGG	TGATAAGCAT	2000
GGAAATAGGA	TTTACTTTT	TAGATGAAAT	AGTACACGGT	GTTCGTTGGG	2050

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ACGCTAAATA	TGCCACTTGG	GATAATTCA	CCGGAAAACC	GGTGACGGT	2100
TATGAAGTAA	ATCGCATTGT	AGGGACATAC	GAGTTGGCTG	AATCGCTTTT	2150
GAAGGCAAAA	GAACGGCTG	CTACCCAAGG	GTACGGATTG	CTTCTATGGG	2200
ACGGTTACCG	TCCTAAGCGT	GCTGTAAACT	GTTTTATGCA	ATGGGCTGCA	2250
CAGCCGGAAA	ATAAACCTGAC	AAAGGAAAAGT	TATTATCCCA	ATATTGACCG	2300
AACTGAGATG	ATTTCAAAAG	GATACGTGGC	TTCAAAATCA	AGCCATAGCC	2350
GCGGCAGTGC	CATTGATCTT	ACGCTTTATC	GATTAGACAC	GGGTGAGCTT	2400
GTACCAATGG	GGAGCCGATT	TGATTTTATG	GATGAACGCT	CTCATCATGC	2450
GGCAAATGGA	ATATCATGCA	ATGAAGCGCA	AAATCGCAGA	CGTTTGCGCT	2500
CCATCATGGA	AAACAGTGGG	TTTGAAGCAT	ATAGCCTCGA	ATGGTGGCAC	2550
TATGTATTAA	GAGACGAACC	ATACCCCAAT	AGCTATTTG	ATTTCCCCGT	2600
					2607
TAAATAA					

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1288 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

GGATCCATCA	GGCAACGACG	GGCTGCTGCC	GGCCATCAGC	GGACGCAGGG	50
AGGACTTTCC	GCAACCGGCC	GTTCGATGCG	GCACCGATGG	CCTTCGCGCA	100
GGGGTAGTGA	ATCCGCCAGG	ATTGACTTGC	GCTGCCCTAC	CTCTCACTAG	150
TGAGGGGGCGG	CAGCGCATCA	AGCGGTGAGC	GCACCTCCGGC	ACCGCCAACT	200
TTCAGCACAT	GGGTGTAAT	CATCGTCGTA	GAGACGTCGG	AATGGCCGAG	250
CAGATCCTGC	ACGGTTCGAA	TGTCGTAACC	GCTGCGGAGC	AAGGCCGTCG	300
CGAACGAGTG	GGGGAGGGTG	TGCGGTGTGG	CGGGCTTCGT	GATGCCTGCT	350
TGTTCTACGG	CACGTTGAA	GGCGCCGTGA	AAGGTCTGGT	CATACATGTG	400
ATGGCGACGC	ACGACACCGC	TCCGTGGATC	GGTCGAATGC	GTGTGCTGCG	450
CAAAAACCCA	GAACCACGGC	CAGGAATGCC	CGGCGCGCGG	ATACTTCCGC	500
TCAAGGGCGT	CGGGAAAGCGC	AACGCCGCTG	CGGCCCTCGG	CCTGGTCCCT	550
CAGCCACCAT	GCCCCTGCAC	GCGACAGCTG	CTCGCGCAGG	CTGGGTGCCA	600
AGCTCTCGGG	TAACATCAAG	GCCCGATCCT	TGGAGCCCTT	GCCCTCCCGC	650
ACGGATGATCG	TGCCGTGATC	GAAATCCAGA	TCCTTGACCC	GCAGTTGCAA	700
ACCCCTCACTG	ATCCGCATGC	CCGTTCCATA	CAGAAGCTGG	GCGAACAAAC	750
GATGCTCGCC	TTCCAGAAAA	CCGAGGATGC	GAACCACCTTC	ATCCGGGGTC	800
AGCACCACCG	GCACCCCG	TCCTTGACCC	TCTCCTGAAG	TCTCCTGAAG	850

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CCAGGGCAGA	TCCGTGCACA	GCACCTTGCC	GTAGAAGAAC	AGCAAGGCCG	900
CCAATGCCTG	ACGATGCGTG	GAGACCGAAA	CCTTGCCTC	GTTCGCCAGC	950
CAGGACAGAA	ATGCCTCGAC	TTCGCTGCTG	CCCAAGGTTG	CCGGGTGACG	1000
CACACCGTGG	AAACGGATGA	AGGCACGAAC	CCAGTGGACA	TAAGCCTGTT	1050
CGGTTCGTAA	GCTGTAATGC	AAGTAGCGTA	TGCGCTCACG	CAACTGGTCC	1100
AGAACCTTGA	CCGAACGCAG	CGGTGGTAAC	GGCGCAGTGG	CGGTTTCAT	1150
GGCTTGTAT	GACTGTTTTT	TTGTACAGTC	TATGCCTCGG	GCATCCAAGC	1200
AGCAAGCGCG	TTACGCCGTG	GGTCGATGTT	TGATGTTATG	GAGCAGCAAC	1250
GATGTTACGC	AGCAGGGCAG	TCGCCCTAAA	ACAAAGTT		1288

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1650 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

GTTAGATGCA	CTAACGACAT	AATTGCTCAC	AGCCAAACTA	TCAGGTCAAG	50
TCTGCTTTA	TTATTTTAA	CGGTGCATAA	TAAGCCCTAC	ACAAATTGGG	100
AGATATATCA	TGAAAGGCTG	GCTTTTCTT	GTTATCGCAA	TAGTTGGCGA	150
AGTAATCGCA	ACATCCGCAT	TAAAATCTAG	CGAGGGCTTT	ACTAAGCTTG	200
CCCCTTCCGC	CGTTGTCATA	ATCGGTTATG	GCATCGCATT	TTATTTCTT	250
TCTCTGGTTC	TGAAATCCAT	CCCTGTCGGT	GTTGCTTATG	CAGTCTGGTC	300
GGGACTCGGC	GTCGTCATAA	TTACAGCCAT	TGCCTGGTTG	CTTCATGGGC	350
AAAAGCTTGA	TGCGTGGGGC	TTTGTAGGTA	TGGGGCTCAT	AATTGCTGCC	400
TTTTTGCTCG	CCCGATCCCC	ATCGTGAAG	TCGCTGCGGA	GGCCGACGCC	450
ATGGTGACGG	TGTTCGGCAT	TCTGAATCTC	ACCGAGGACT	CCTTCTTCGA	500
TGAGAGCCGG	CGGCTAGACC	CCGCCGGCGC	TGTCACCGCG	GCGATCGAAA	550
TGCTGCGAGT	CGGATCAGAC	GTCGTGGATG	TCGGACCGGC	CGCCAGCCAT	600
CCGGACGCGA	GGCCTGTATC	GCCGGCCGAT	GAGATCAGAC	GTATTGCGCC	650
GCTCTTAGAC	GCCCTGTCCG	ATCAGATGCA	CCGTGTTCA	ATCGACAGCT	700
TCCAACCGGA	AACCCAGCGC	TATGCGCTCA	AGCGCGGGGT	GGGCTACCTG	750
AACGATATCC	AAGGATTTC	TGACCCCTGCG	CTCTATCCCG	ATATTGCTGA	800
GGCGGACTGC	AGGCTGGTGG	TTATGCACTC	AGCGCAGCGG	GATGGCATCG	850
CCACCCGCAC	CGGTCACCTT	CGACCCGAAG	ACCGCGCTCGA	CGAGATTGTG	900
CGGTTCTTCG	AGGCGCGGGT	TTCCGCTTGT	CGACGGAGCG	GGGTGCGTGC	950
CGACCGGGCTC	ATCCTCGATC	CGGGGATGGG	ATTTTCTTG	AGCCCCGCAC	1000

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CGGAAACATC	GCTGCACGTG	CTGTCGAACC	TTCAAAAGCT	GAAGTCGGCG	1050
TTGGGGCTTC	CGCTATTGGT	CTCGGTGTCG	CGGAAATCCT	TCTTGGCGC	1100
CACCGTTGGC	CTTCCTGTAA	AGGATCTGGG	TCCAGCGAGC	CTTGCAGCGG	1150
AACTTCACGC	GATCGGCAAT	GGCGCTGACT	ACGTCCGCAC	CCACGCGCCT	1200
GGAGATCTGC	GAAGCGCAAT	CACCTTCTCG	AAAACCTCG	CGAAATTTCG	1250
CAGTCGCGAC	GCCAGAGACC	GAGGGTTAGA	TCATGCCTAG	CATTACACCTT	1300
CCGGCCGCC	GCTAGCGGAC	CCTGGTCAGG	TTCCCGGAAG	GTGGGCGCAG	1350
ACATGCTGGG	CTCGTCAGGA	TCAAACGTCA	CTATGAGGCG	GCGGTTCAT	1400
CCGCGCCAGG	GGAGCGAATG	GACAGCGAGG	AGCCTCCGAA	CGTCGGGTC	1450
GCCTGCTCGG	GTGATATCGA	CGAGGTTGTG	CGGCTGATGC	ACGACGCTGC	1500
GGCGTGGATG	TCCGCCAAGG	GAACGCCGC	CTGGGACGTC	GCGCGGATCG	1550
ACCGGACATT	CGCGGAGACC	TTCGTCTGA	GATCCGAGCT	CCTAGTCGCG	1600
AGTTGCAGCG	ACGGCATTGT	CGGCTGTTGC	ACCTTGTCGG	CCGAGGATCC	1650

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

ATGGGTCCGA	ATCCTATGAA	AATGTATCCT	ATAGAAGGAA	ACAAATCAGT	50
ACAATTATC	AAACCTATTT	TAGAAAAATT	AGAAAATGTT	GAGGTTGGAG	100
AAATACTCATA	TTATGATTCT	AAGAATGGAG	AAACTTTGA	TAAGCAAATT	150
TTATATCATT	ATCCAATCTT	AAACGATAAG	TTAAAAATAG	GTAAATTTG	200
CTCAATAGGA	CCAGGTGTAA	CTATTATTAT	GAATGGAGCA	AATCATAGAA	250
TGGATGGCTC	AACATATCCA	TTTAATTAT	TTGGTAATGG	ATGGGAGAAA	300
CATATGCCAA	AATTAGATCA	ACTACCTATT	AAGGGGGATA	CAATAATAGG	350
TAATGATGTA	TGGATAGGAA	AAGATGTTGT	AATTATGCCA	GGAGTAAAAA	400
TCGGGGATGG	TGCAATAGTA	GCTGCTAATT	CTGTTGTTGT	AAAAGATATA	450
GCCCCATACA	TGTTAGCTGG	AGGAAATCCT	GCTAACGAAA	TAAAACAAAG	500
ATTTGATCAA	GATACAATAA	ATCAGCTGCT	TGATATAAAA	TGGTGGATT	550
GGCCAATAGA	CATTATTAAT	GAGAATATAG	ATAAAATTCT	TGATAATAGC	600
ATCATTAGAG	AAGTCATATG	GAAGAAATGA			630

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1440 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

ATGAATATAG	TTGAAAATGA	AATATGTATA	AGAACTTTAA	TAGATGATGA	50
TTTTCCCTTG	ATGTTAAAAT	GGTTAACTGA	TGAAAAGAGTA	TTAGAATTAA	100
ATGGTGGTAG	AGATAAAAAAA	TATACATTAG	AATCATTAAA	AAAACATTAT	150
ACAGAGCCTT	GGGAAGATGA	AGTTTTAGA	GTAATTATTG	AATATAACAA	200
TGTTCCCTATT	GGATATGGAC	AAATATATAA	AATGTATGAT	GAGTTATATA	250
CTGATTATCA	TTATCCAAAA	ACTGATGAGA	TAGTCTATGG	TATGGATCAA	300
TTTATAGGAG	AGCCAAATTA	TTGGAGTAAA	GGAATTGGTA	CAAGATATAT	350
TAAATTGATT	TTTGAATTAA	TGAAAAAAGA	AAGAAATGCT	AATGCAGTTA	400
TTTTAGACCC	TCATAAAAAT	AATCCAAGAG	CAATAAGGGC	ATACCAAAAA	450
TCTGGTTTTA	GAATTATTGA	AGATTGCCA	GAACATGAAT	TACACGGAGG	500
CAAAAAAGAA	GATTGTTATT	TAATGGAATA	TAGATATGAT	GATAATGCCA	550
CAAATGTTAA	GGCAATGAAA	TATTTAATTG	AGCATTACTT	TGATAATTTC	600
AAAGTAGATA	GTATTGAAAT	AATCGGTAGT	GGTTATGATA	GTGTGGCATA	650
TTTAGTTAAT	AATGAATACA	TTTTAAAAC	AAAATTAGT	ACTAATAAGA	700
AAAAAGGTAA	TGCAAAAGAA	AAAGCAATAT	ATAATTTCAT	AAATACAAAT	750
TTAGAAACTA	ATGTTAAAAT	TCCTAATATT	GAATATTGCT	ATATTAGTGA	800
TGAATTATCT	ATACTAGGTT	ATAAAGAAAT	TAAAGGAACT	TTTTAACAC	850
CAGAAATTAA	TTCTACTATG	TCAGAAGAAG	AACAAAATT	GTTAAAACGA	900
GATATTGCCA	GTTTTTAAG	ACAAATGCAC	GGTTTAGATT	ATACAGATAT	950
TAGTGAATGT	ACTATTGATA	ATAAACAAA	TGTATTAGAA	GAGTATATAT	1000
TGTTGCGTGA	AACTATTAT	AATGATTAA	CTGATATAGA	AAAAGATTAT	1050
ATAGAAAGTT	TTATGGAAAG	ACTAAATGCA	ACAACAGTT	TTGAGGGTAA	1100
AAAGTGTAA	TGCCATAATG	ATTTTAGTTG	TAATCATCTA	TTGTTAGATG	1150
GCAATAATAG	ATTAACGGA	ATAATTGATT	TTGGAGATTC	TGGAATTATA	1200
GATGAATATT	GTGATTAAAT	ATACTTACTT	GAAGATAGTG	AAGAAGAAAT	1250
AGGAACAAAT	TTTGGAGAAG	ATATATTAAG	AATGTATGGA	AATATAGATA	1300
TTGAGAAAGC	AAAAGAATAT	CAAGATATAG	TTGAAGAATA	TTATCCTATT	1350
GAAACTATTG	TTTATGGAAT	TAAAAATATT	AAACAGGAAT	TTATCGAAAA	1400
TGGTAGAAAAA	GAAATTATA	AAAGGACTTA	AAAAGATTGA		1440

(2) INFORMATION FOR SEQ ID NO: 175:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

TTGAATTTAA	ACAATGACCA	TGGACCTGAT	CCCGAAAATA	TTTTACCGAT	50
AAAAGGGAAT	CGGAATCTTC	AATTTATAAA	ACCTACTATA	ACGAACGAAA	100
ACATTTGGT	GGGGGAATAT	TCTTATTATG	ATAGTAAGCG	AGGAGAATCC	150
TTTGAAGATC	AAGTCTTATA	TCATTATGAA	GTGATTGGAG	ATAAGTTGAT	200
TATAGGAAGA	TTTTGTTCAA	TTGGTCCCGG	AACAACATTT	ATTATGAATG	250
GTGCAAACCA	TCGGATGGAT	GGATCAACAT	ATCCTTTCA	TCTATTCAAGG	300
ATGGGTTGGG	AGAAGTATAT	GCCTTCCTTA	AAAGATCTTC	CCTTGAAAGG	350
GGACATTGAA	ATTGGAAATG	ATGTATGGAT	AGGTAGAGAT	GTAACCATTA	400
TGCCCTGGGT	AAAAATTGGG	GACGGGCAA	TCATTGCTGC	AGAAGCTGTT	450
GTCACAAAGA	ATGTTGCTCC	CTATTCTATT	GTCGGTGGAA	ATCCCTTAAA	500
ATTTATAAGA	AAAAGGTTT	CTGATGGAGT	TATCGAAGAA	TGGTTAGCTT	550
TACAATGGTG	GAATTAGAT	ATGAAAATTA	TTAATGAAAA	TCTTCCCTTC	600
ATAATAATG	GAGATATCGA	AATGCTGAAG	AGAAAAAGAA	AACTTCTAGA	650
TGACACTTGA					660

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1569 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

ATGAAAATAA	TGTTAGAGGG	ACTTAATATA	AAACATTATG	TTCAAGATCG	50
TTTATTGTTG	AACATAAATC	GCCTAAAGAT	TTATCAGAAT	GATCGTATTG	100
GTTTAATTGG	TAAAATGGA	AGTGGAAAAAA	CAACGTTACT	TCACATATTA	150
TATAAAAAAA	TTGTGCCTGA	AGAAGGTATT	GTAAAACAAT	TTTCACATTG	200
TGAACTTATT	CCTCAATTGA	AGCTCATAGA	ATCAACTAAA	AGTGGTGGTG	250
AAGTAACACG	AAACTATATT	CGGCAAGCGC	TTGATAAAAA	TCCAGAACTG	300
CTATTAGCAG	ATGAACCAAC	AACCTTGTAA	GGAAACAGG	TTATAGAAAA	350

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ATAGAACAG	GATTTAAAAA	ATTGGCATGG	AGCATTATT	ATAGTTCAC	400
ATGATCGCGC	TTTTTTAGAT	AACTTGTGTA	CTACTATATG	GGAAATTGAC	450
GAGGGAAAGAA	TAACGTAAATA	TAAGGGGAAT	TATAGTAACT	ATGTTGAACA	500
AAAAGAATTA	GAAAGACATC	GAGAAGAATT	AGAATATGAA	AAATATGAAA	550
AAGAAAAGAA	ACGATTGGAA	AAAGCTATAA	ATATAAAAGA	ACAGAAAGCT	600
CAACGAGCAA	CTAAAAAACCC	GAAAAACTTA	AGTTTATCTG	AAGGCAAAAT	650
AAAAGGAGCA	AAGCCATACT	TTGCAGGTAA	GCAAAAGAAG	TTACGAAAAA	700
CTGTAAAATC	TCTAGAAACC	AGACTAGAAA	AACTTGAAAG	CGTCGAAAAG	750
AGAAACGAAC	TTCCCTCCACT	TAAAATGGAT	TTAGTGAACT	TAGAAAGTGT	800
AAAAAAATAGA	ACTATAATAC	GTGGTGAAGA	TGTCTCGGGT	ACAATTGAAG	850
GACGGGTATT	GTGGAAAGCA	AAAAGTTTA	GTATTCGCGG	AGGAGACAAG	900
ATGGCAATT	TCGGATCTAA	TGGTACAGGA	AAGACAACGT	TTATTAAGAA	950
AATTGTGCAT	GGGAATCCTG	GTATTTCATT	ATGCCATCT	GTCAAAATCG	1000
GTTATTTAG	CCAAAAAATA	GATACATTAG	AATTAGATAA	GAGCATTAA	1050
GAAAATGTT	AATCTTCTTC	ACAACAAAAT	GAAACTCTTA	TTCGAACTAT	1100
TCTAGCTAGA	ATGCATTTTT	TTAGAGATGA	TGTTTATAAA	CCAATAAGTG	1150
TCTTAAGTGG	TGGAGAGCGA	GTTAAAGTAG	CACTAACTAA	AGTATTCTTA	1200
AGTGAAGTTA	ATACGTTGGT	ACTAGATGAA	CCAACAAACT	TTCTTGATAT	1250
GGAAGCTATA	GAGGCCGTTG	AATCTTGT	AAAGGAATAT	AATGGCAGTA	1300
TAATCTTGT	ATCTCACGAT	CGTAAATT	TCGAAAAAGT	AGCCACTCGA	1350
ATAATGACAA	TTGATAATAA	AGAAAATAAA	ATATTTGATG	GCACATATGA	1400
ACAATTTAAA	CAAGCTGAAA	AGCCAACAAG	GAATATTAAA	GAAGATAAAA	1450
AACTTTTACT	TGAGACAAAAA	ATTACAGAAG	TACTCAGTCG	ATTGAGTATT	1500
GAACCTTCGG	AAGAATTAGA	ACAAGAGTTT	CAAAACTAA	TAAATGAAAA	1550
AAGAAATTG	GATAAATAA				1569

(2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1467 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Double
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

ATGGAACAAT	ATACAATTAA	ATTTAACCAA	ATCAATCATA	AATTGACAGA	50
TTTACGATCA	CTTAACATCG	ATCATTTTA	TGCTTACCAA	TTTGAAAAAA	100

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TAGCACTTAT	TGGGGGTAAT	GGTACTGGTA	AAACCACATT	ACTAAATATG	150
ATTGCTAAA	AAACAAAACC	AGAATCTGGA	ACAGTTGAAA	CGAATGGCGA	200
AATTCAATAT	TTTGAACAGC	TTAACATGGA	TGTGGAAAAT	GATTTAACCA	250
CGTTAGACGG	TAGTTAATG	AGTGAACCTCC	ATATAACCTAT	GCATACAACC	300
GACAGTATGA	GTGGTGGTGA	AAAAGCAAAA	TATAAATTAC	GTAATGTCAT	350
ATCAAATTAT	AGTCCGATAT	TACTTTAGA	TGAACCTACA	AATCACTTGG	400
ATAAAATTGG	TAAAGATTAT	CTGAATAATA	TTTTAAAATA	TTACTATGGT	450
ACTTTAATT	TAGTAAGTCA	CGATAGAGCA	CTTATAGACC	AAATTGCTGA	500
CACAATTG	GATATACAAG	AAGATGGCAC	AATAAGAGTG	TTTAAAGGTA	550
ATTACACACA	GTATCAAAAT	CAATATGAAC	AAGAACAGTT	AGAACAAACAA	600
CGTAAATATG	AACAGTATAT	AAGTAAAAAA	CAAAGATTGT	CCCAAGCCAG	650
TAAAGCTAAA	CGAAATCAAG	CGCAACAAAT	GGCACAAGCA	TCATCAAAAC	700
AAAAAAATAA	AAGTATAGCA	CCAGATCGTT	TAAGTGCATC	AAAAGAAAAA	750
GGCACGGTTG	AGAAGGCTGC	TCAAAAACAA	GCTAAGCATA	TTGAAAAAAG	800
AATGGAACAT	TTGGAAAGAAG	TTGAAAAAACC	ACAAAGTTAT	CATGAATTCA	850
ATTTTCCACA	AAATAAAATT	TATGATATCC	ATAATAATT	TCCAATCATT	900
GCACAAATC	TAACATTGGT	TAAAGGAAGT	CAAAAACGT	TAACACAAAGT	950
ACGATTCCAA	ATACCATATG	GCAAAAATAT	ACCGCTCGTA	GGTGCACATG	1000
GTGTAGGTAA	GACAACTTA	CTTGAAGCTA	TTTACCCACCA	AATAGAGGGA	1050
ATTGATTGTT	CTCCTAAAGT	GCAAATGGCA	TACTATCGTC	AACTTGCTTA	1100
TGAAGACATG	CGTGACGTTT	CATTATTGCA	ATATTTAATG	GATGAAACGG	1150
ATTCATCAGA	ATCATTCACT	AGAGCTATTT	TAAATAACTT	GGGTTAAAT	1200
GAAGCACTTG	AGCGTTCTTG	TAATGTTTG	AGTGGTGGGG	AAAGAACGAA	1250
ATTATCGTTA	GCAGTATTAT	TTTCAACGAA	AGCGAATATG	TTAATTTGG	1300
ATGAACCAAC	TAATTTTTA	GATATTAATAA	CATTAGAACG	ATTAGAAATG	1350
TTTATGAATA	AATATCCTGG	AATCATTG	TTTACATCAC	ATGATACAAG	1400
GTTTGTAA	CATGTATCAG	ATAAAAAATG	GGAATTAACA	GGACAATCTA	1450
TTCATGATAT	AACTTAA				1467

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CLAIMSWhat is claimed is:

1. A method using probes (fragments and/or oligonucleotides) and/or amplification primers which are specific, ubiquitous and sensitive for determining the presence and/or amount of nucleic acids from bacterial species selected from the group consisting of *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Enterococcus faecalis*, *Staphylococcus saprophyticus*, *Streptococcus pyogenes*, *Haemophilus influenzae* and *Moraxella catarrhalis* in any sample suspected of containing said bacterial nucleic acid, wherein said bacterial nucleic acid or variant or part thereof comprises a selected target region hybridizable with said probes or primers; said method comprising the steps of contacting said sample with said probes or primers and detecting the presence and/or amount of hybridized probes and/or amplified products as an indication of the presence and/or amount of said bacterial species.
2. A method as defined in claim 1 further using probes (fragments and/or oligonucleotides) and/or amplification primers which are universal and sensitive for determining the presence and/or amount of nucleic acids from any bacteria from any sample suspected of containing said bacterial nucleic acid, wherein said bacterial nucleic acid or variant or part thereof comprises a selected target region hybridizable with said probes or primers; said method comprising the steps of contacting said sample with said probes or primers and detecting the presence and/or amount of hybridized probes and/or amplified products as an indication of the presence and/or amount of said any bacteria.
3. A method as defined in claim 1 further using probes (fragments and/or oligonucleotides) and/or amplification primers which are specific, ubiquitous and sensitive for

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determining the presence and/or amount of nucleic acids from an antibiotic resistance gene selected from the group consisting of *blatem*, *Blarob*, *Blashv*, *aadB*, *aacC1*, *aacC2*, *aacC3*, *aacA4*, *mecA*, *vanA*, *vanH*, *vanX*, *satA*, *aacA-aphD*, *vat*, 5 *vga*, *msrA*, *sul* and *int* in any sample suspected of containing said bacterial nucleic acid, wherein said bacterial nucleic acid or variant or part thereof comprises a selected target region hybridizable with said probes or primers; said method comprising the steps of contacting said sample with said 10 probes or primers and detecting the presence and/or amount of hybridized probes and/or amplified products as an indication of the presence and/or amount of said antibiotic resistance gene.

15 4. The method of any one of claims 1, 2 and 3 which is performed directly on a sample obtained from human patients, animals, environment or food.

20 5. The method of any one of claims 1, 2 and 3 which is performed directly on a sample consisting of one or more bacterial colonies.

25 6. The method of any one of claims 1 to 5, wherein the bacterial nucleic acid is amplified by a method selected from the group consisting of:

- a) polymerase chain reaction (PCR),
- b) ligase chain reaction,
- c) nucleic acid sequence-based amplification,
- d) self-sustained sequence replication,
- 30 e) strand displacement amplification,
- f) branched DNA signal amplification,
- g) nested PCR, and
- h) multiplex PCR.

35 7. The method of claim 6 wherein said bacterial nucleic acid is amplified by PCR.

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8. The method of claim 7 wherein the PCR protocol is modified to determine within one hour the presence of said bacterial nucleic acids by performing for each amplification cycle an annealing step of only one second at 55°C and a 5 denaturation step of only one second at 95°C without any elongation step.

9. A method for the detection, identification and/or quantification of *Escherichia coli* directly from a test sample 10 or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from 15 this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

20 said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group 25 consisting of SEQ ID NO:3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Escherichia coli*, under conditions such that the nucleic acid 30 of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member 35 reacting with a second reactive member present on said probe; and

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c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Escherichia coli* in said test sample.

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10. A method as defined in claim 9, wherein said probe is selected from the group consisting of:

10 1) an oligonucleotide of 12-227 nucleotides in length which sequence is comprised in SEQ ID NO: 3 or a complementary sequence thereof,

15 2) an oligonucleotide of 12-278 nucleotides in length which sequence is comprised in SEQ ID NO: 4 or a complementary sequence thereof;

15 3) an oligonucleotide of 12-1596 nucleotides in length which sequence is comprised in SEQ ID NO: 5 or a complementary sequence thereof,

20 4) an oligonucleotide of 12-2703 nucleotides in length which sequence is comprised in SEQ ID NO: 6 or a complementary sequence thereof,

20 5) an oligonucleotide of 12-1391 nucleotides in length which sequence is comprised in SEQ ID NO: 7 or a complementary sequence thereof, and

25 variants thereof which specifically and ubiquitously anneal with strains and representatives of *Escherichia coli*.

25

30 11. The method of claim 10, wherein the probe for detecting nucleic acid sequences from *Escherichia coli* is selected from the group consisting of SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, SEQ ID NO: 54 and a sequence complementary thereof..

35 12. A method for detecting the presence and/or amount of *Escherichia coli* in a test sample which comprises the following steps:

35 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having

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at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Escherichia coli* DNA that contains a target sequence, and the other of said primers being capable 5 of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6 and SEQ ID NO: 7;

10 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

15 c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Escherichia coli* in said test sample.

13. The method of claim 12, wherein said at least one pair of primers is selected from the group consisting of:

20 a) SEQ ID NO: 42 and SEQ ID NO: 43,
b) SEQ ID NO: 46 and SEQ ID NO: 47,
c) SEQ ID NO: 55 and SEQ ID NO: 56, and
d) SEQ ID NO: 131 and SEQ ID NO: 132.

25 14. A method for the detection, identification and/or quantification of *Klebsiella pneumoniae* directly from a test sample or from bacterial colonies, which comprises the following steps:

30 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

35 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA.

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said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid 5 which nucleotidic sequence is selected from the group consisting of SEQ ID NO:8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Klebsiella pneumoniae*, 10 under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said 15 labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Klebsiella pneumoniae* in said 20 test sample.

15. A method as defined in claim 14, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-238 nucleotides in length 25 which sequence is comprised in SEQ ID NO: 8 or a complementary sequence thereof,

2) an oligonucleotide of 12-385 nucleotides in length which sequence is comprised in SEQ ID NO: 9 or a complementary sequence thereof,

30 3) an oligonucleotide of 12-462 nucleotides in length which sequence is comprised in SEQ ID NO: 10 or a complementary sequence thereof,

35 4) an oligonucleotide of 12-730 nucleotides in length which sequence is comprised in SEQ ID NO: 11 or a complementary sequence thereof, and

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variants thereof which specifically and ubiquitously anneal with strains and representatives of *Klebsiella pneumoniae*.

5 16. The method of claim 15, wherein the probe for detecting nucleic acid sequences from *Klebsiella pneumoniae* is selected from the group consisting of SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 69 and a sequence 10 complementary thereof.

17. A method for detecting the presence and/or amount of *Klebsiella pneumoniae* in a test sample which comprises the following steps:

15 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Klebsiella pneumoniae* DNA that 20 contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ 25 ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, and SEQ ID NO: 11;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

30 c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Klebsiella pneumoniae* in said test sample.

18. The method of claim 17, wherein said at least one pair of 35 primers is selected from the group consisting of:

a) SEQ ID NO: 61 and SEQ ID NO: 62,

b) SEQ ID NO: 67 and SEQ ID NO: 68

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- c) SEQ ID NO: 135 and SEQ ID NO: 136, and
- d) SEQ ID NO: 137 and SEQ ID NO: 138.

19. A method for the detection, identification and/or quantification of *Proteus mirabilis* directly from a test sample or from bacterial colonies, which comprises the following steps:

5 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a 10 substantially homogenous population of bacteria isolated from this sample, or

15 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

20 said bacterial DNA being in a substantially single stranded form;

25 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Proteus mirabilis*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said 30 labelling means, said first reactive member reacting with a second reactive member present on said probe; and

35 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Proteus mirabilis* in said test sample.

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20. A method as defined in claim 19, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-225 nucleotides in length which sequence is comprised in SEQ ID NO: 12 or a 5 complementary sequence thereof,

2) an oligonucleotide of 12-402 nucleotides in length which sequence is comprised in SEQ ID NO: 13 or a complementary sequence thereof,

3) an oligonucleotide of 12-157 nucleotides in length 10 which sequence is comprised in SEQ ID NO: 14 or a complementary sequence thereof,

4) an oligonucleotide of 12-1348 nucleotides in length which sequence is comprised in SEQ ID NO: 15 or a complementary sequence thereof, and

15 variants thereof which specifically and ubiquitously anneal with strains and representatives of *Proteus mirabilis*.

21. The method of claim 20, wherein the probe for detecting nucleic acid sequences from *Proteus mirabilis* is selected from 20 the group consisting of SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82 and a sequence complementary thereof.

25 22. A method for detecting the presence and/or amount of *Proteus mirabilis* in a test sample which comprises the following steps:

30 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Proteus mirabilis* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an 35 extension product which contains the target sequence as a template, said at least one pair of primers being chosen from

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within one of the following sequences: SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, and SEQ ID NO: 15;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence,

5 and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Proteus mirabilis* in said test sample.

10

23. The method of claim 22, wherein said at least one pair of primers is selected from the group consisting of:

- a) SEQ ID NO: 74 and SEQ ID NO: 75, and
- b) SEQ ID NO: 133 and SEQ ID NO: 134.

15

24. A method for the detection, identification and/or quantification of *Staphylococcus saprophyticus* directly from a test sample or from bacterial colonies, which comprises the following steps:

20 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

25 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

30 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Staphylococcus saprophyticus*, under conditions such that the nucleic acid of

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said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of 5 said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Staphylococcus saprophyticus* in 10 said test sample.

25. A method as defined in claim 24, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-172 nucleotides in length 15 which sequence is comprised in SEQ ID NO: 21 or a complementary sequence thereof,

2) an oligonucleotide of 12-155 nucleotides in length which sequence is comprised in SEQ ID NO: 22 or a complementary sequence thereof,

20 3) an oligonucleotide of 12-145 nucleotides in length which sequence is comprised in SEQ ID NO: 23 or a complementary sequence thereof,

4) an oligonucleotide of 12-265 nucleotides in length 25 which sequence is comprised in SEQ ID NO: 24 or a complementary sequence thereof, and variants thereof which specifically and ubiquitously anneal with strains and representatives of *Staphylococcus saprophyticus*.

30 26. The method of claim 25, wherein the probe for detecting nucleic acid sequences from *Staphylococcus saprophyticus* is selected from the group consisting of SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104 and a sequence complementary thereof.

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27. A method for detecting the presence and/or amount of *Staphylococcus saprophyticus* in a test sample which comprises the following steps:

5 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Staphylococcus saprophyticus* DNA that contains a target sequence, and the other of said primers 10 being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, and SEQ ID NO: 24;

15 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

20 c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Staphylococcus saprophyticus* in said test sample.

28. The method of claim 27, wherein said at least one pair of primers is selected from the group consisting of:

25 a) SEQ ID NO: 98 and SEQ ID NO: 99, and

b) SEQ ID NO: 139 and SEQ ID NO: 140.

29. A method for the detection, identification and/or quantification of *Moraxella catarrhalis* directly from a test 30 sample or from bacterial colonies, which comprises the following steps:

35 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert

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support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

- 5 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 28, SEQ ID NO: 29, a sequence complementary thereof, a part thereof and a variant thereof,
10 which specifically and ubiquitously anneals with strains or representatives of *Moraxella catarrhalis*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling
15 means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and
- 20 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Moraxella catarrhalis* in said test sample.

30. A method as defined in claim 29, wherein said probe is selected from the group consisting of:

- 25 1) an oligonucleotide of 12-526 nucleotides in length which sequence is comprised in SEQ ID NO: 28 or a complementary sequence thereof,
- 30 2) an oligonucleotide of 12-466 nucleotides in length which sequence is comprised in SEQ ID NO: 29 or a complementary sequence thereof, and variants thereof which specifically and ubiquitously anneal with strains and representatives of *Moraxella catarrhalis*.

35 31. The method of claim 30, wherein the probe for detecting nucleic acid sequences from *Moraxella catarrhalis* is selected

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from the group consisting of SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117 and a sequence complementary thereof.

5

32. A method for detecting the presence and/or amount of *Moraxella catarrhalis* in a test sample which comprises the following steps:

- 10 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Moraxella catarrhalis* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 28 and SEQ ID NO: 29;
- 20 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and
- 25 c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Moraxella catarrhalis* in said test sample.

33. The method of claim 32, wherein said at least one pair of primers is selected from the group consisting of:

- 30 a) SEQ ID NO: 112 and SEQ ID NO: 113,
- b) SEQ ID NO: 118 and SEQ ID NO: 119, and
- c) SEQ ID NO: 160 and SEQ ID NO: 119.

34. A method for the detection, identification and/or quantification of *Pseudomonas aeruginosa* directly from a test sample or from bacterial colonies, which comprises the following steps:

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a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

5 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

10 said bacterial DNA being in a substantially single stranded form;

15 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Pseudomonas aeruginosa*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

20 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Pseudomonas aeruginosa* in said test sample.

25 35. A method as defined in claim 34, wherein said probe is selected from the group consisting of:

30 1) an oligonucleotide of 12-2167 nucleotides in length which sequence is comprised in SEQ ID NO: 16 or a complementary sequence thereof,

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2) an oligonucleotide of 12-1872 nucleotides in length which sequence is comprised in SEQ ID NO: 17 or a complementary sequence thereof,

3) an oligonucleotide of 12-3451 nucleotides in length 5 which sequence is comprised in SEQ ID NO: 18 or a complementary sequence thereof,

4) an oligonucleotide of 12-744 nucleotides in length which sequence is comprised in SEQ ID NO: 19 or a complementary sequence thereof,

10 5) an oligonucleotide of 12-2760 nucleotides in length which sequence is comprised in SEQ ID NO: 20 or a complementary sequence thereof, and variants thereof which specifically and ubiquitously anneal with strains and representatives of *Pseudomonas* 15 *aeruginosa*.

36. The method of claim 35, wherein the probe for detecting nucleic acid sequences from *Pseudomonas aeruginosa* is selected from the group consisting of SEQ ID NO: 87, SEQ ID NO: 88, SEQ 20 ID NO: 89, SEQ ID NO: 90, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95 and a sequence complementary thereof.

37. A method for detecting the presence and/or amount of 25 *Pseudomonas aeruginosa* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being 30 capable of hybridizing selectively with one of the two complementary strands of *Pseudomonas aeruginosa* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target 35 sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ

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ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19 and SEQ ID NO: 20;

5 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Pseudomonas aeruginosa* in said test sample.

10

38. The method of claim 37, wherein said at least one pair of primers is selected from the group consisting of:

- a) SEQ ID NO: 83 and SEQ ID NO: 84, and
- b) SEQ ID NO: 85 and SEQ ID NO: 86.

15

39. A method for the detection, identification and/or quantification of *Staphylococcus epidermidis* directly from a test sample or from bacterial colonies, which comprises the following steps:

20 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

25 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

30 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 36, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Staphylococcus epidermidis*, under conditions such that the nucleic acid of said probe can selectively hybridize with said

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bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

5 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Staphylococcus epidermidis* in 10 said test sample.

40. A method as defined in claim 39, wherein said probe is selected from the group consisting of an oligonucleotide of 12-705 nucleotides in length which sequence is comprised in 15 SEQ ID NO: 36 and variants thereof which specifically and ubiquitously anneal with strains and representatives of *Staphylococcus epidermidis*.

41. A method for detecting the presence and/or amount of 20 *Staphylococcus epidermidis* in a test sample which comprises the following steps:

25 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Staphylococcus epidermidis* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target 30 sequence as a template, said at least one pair of primers being chosen from within the following sequence: SEQ ID NO: 36;

35 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

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c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Staphylococcus epidermidis* in said test sample.

5 42. The method of claim 41, wherein said at least one pair of primers is selected from the group consisting of:
a) SEQ ID NO: 145 and SEQ ID NO: 146, and
b) SEQ ID NO: 147 and SEQ ID NO: 148.

10 43. A method for the detection, identification and/or quantification of *Staphylococcus aureus* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving 15 in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

20 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

25 said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 37, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of 30 *Staphylococcus aureus*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

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c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Staphylococcus aureus* in said test sample.

5

44. A method as defined in claim 43, wherein said probe is selected from the group consisting of an oligonucleotide of 12-442 nucleotides in length which sequence is comprised in SEQ ID NO: 37 and variants thereof which specifically and ubiquitously anneal with strains and representatives of *Staphylococcus aureus*.

15

45. A method for detecting the presence and/or amount of *Staphylococcus aureus* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Staphylococcus aureus* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the following sequence: SEQ ID NO: 37;

30

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Staphylococcus aureus* in said test sample.

35 46. The method of claim 45, wherein said at least one pair of primers is selected from the group consisting of:

a) SEQ ID NO: 149 and SEQ ID NO: 150,

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b) SEQ ID NO: 149 and SEQ ID NO: 151, and
c) SEQ ID NO: 152 and SEQ ID NO: 153.

47. A method for the detection, identification and/or
5 quantification of *Haemophilus influenzae* directly from a test
sample or from bacterial colonies, which comprises the
following steps:

10 a) depositing and fixing on an inert support or leaving
in solution the bacterial DNA of the sample or of a
substantially homogenous population of bacteria isolated from
this sample, or

15 inoculating said sample or said substantially homogenous
population of bacteria isolated from this sample on an inert
support, and lysing *in situ* said inoculated sample or isolated
bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single
stranded form;

20 b) contacting said single stranded DNA with a probe, said
probe comprising at least one single stranded nucleic acid
which nucleotidic sequence is selected from the group
consisting of SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, a
sequence complementary thereof, a part thereof and a variant
thereof, which specifically and ubiquitously anneals with
25 strains or representatives of *Haemophilus influenzae*, under
conditions such that the nucleic acid of said probe can
selectively hybridize with said bacterial DNA, whereby a
hybridization complex is formed, said complex being detected
by labelling means, the label being present on said probe or
the label being present on a first reactive member of said
30 labelling means, said first reactive member reacting with a
second reactive member present on said probe; and

35 c) detecting the presence or the intensity of said label
on said inert support or in said solution as an indication of
the presence and/or amount of *Haemophilus influenzae* in said
test sample.

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48. A method as defined in claim 47, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-845 nucleotides in length which sequence is comprised in SEQ ID NO: 25 or a 5 complementary sequence thereof,

2) an oligonucleotide of 12-1598 nucleotides in length which sequence is comprised in SEQ ID NO: 26 or a complementary sequence thereof,

3) an oligonucleotide of 12-9100 nucleotides in length 10 which sequence is comprised in SEQ ID NO: 27 or a complementary sequence thereof, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Haemophilus influenzae*.

15

49. The method of claim 48, wherein the probe for detecting nucleic acid sequences from *Haemophilus influenzae* is selected from the group consisting of SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107 and a sequence complementary thereof.

20

50. A method for detecting the presence and/or amount of *Haemophilus influenzae* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution 25 containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Haemophilus influenzae* DNA that contains a target sequence, and the other of said primers 30 being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 25, SEQ ID NO: 26 and SEQ ID NO: 27;

35 b) synthesizing an extension product of each of said primers which extension products contain the target sequence,

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and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Haemophilus influenzae* in said test sample.

5 51. The method of claim 50, wherein said at least one pair of primers comprises the following pair: SEQ ID NO: 154 and SEQ ID NO: 155.

10 52. A method for the detection, identification and/or quantification of *Streptococcus pneumoniae* directly from a test sample or from bacterial colonies, which comprises the following steps:

15 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

20 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

25 said bacterial DNA being in a substantially single stranded form;

30 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 34, SEQ ID NO: 35, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Streptococcus pneumoniae*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being

35 detected by labelling means, the label being present on said probe or the label being present on a first reactive member of

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said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

5 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Streptococcus pneumoniae* in said test sample.

53. A method as defined in claim 52, wherein said probe is selected from the group consisting of:

10 1) an oligonucleotide of 12-631 nucleotides in length which sequence is comprised in SEQ ID NO: 30 or a complementary sequence thereof,

15 2) an oligonucleotide of 12-3754 nucleotides in length which sequence is comprised in SEQ ID NO: 31 or a complementary sequence thereof,

3) an oligonucleotide of 12-841 nucleotides in length which sequence is comprised in SEQ ID NO: 34 or a complementary sequence thereof,

20 4) an oligonucleotide of 12-4500 nucleotides in length which sequence is comprised in SEQ ID NO: 35 or a complementary sequence thereof, and variants thereof which specifically and ubiquitously anneal with strains and representatives of *Streptococcus pneumoniae*.

25 54. The method of claim 53, wherein the probe for detecting nucleic acid sequences from *Streptococcus pneumoniae* is selected from the group consisting of SEQ ID NO: 120, SEQ ID NO: 121 and a sequence complementary thereof.

30 55. A method for detecting the presence and/or amount of *Streptococcus pneumoniae* in a test sample which comprises the following steps:

35 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two

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complementary strands of *Streptococcus pneumoniae* DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target 5 sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 34 and SEQ ID NO: 35;

10 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

15 c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Streptococcus pneumoniae* in said test sample.

56. The method of claim 55, wherein said at least one pair of primers is selected from the group consisting of:

- 15 a) SEQ ID NO: 78 and SEQ ID NO: 79,
- 16 b) SEQ ID NO: 156 and SEQ ID NO: 157, and
- 20 c) SEQ ID NO: 158 and SEQ ID NO: 159.

57. A method for the detection, identification and/or quantification of *Streptococcus pyogenes* directly from a test sample or from bacterial colonies, which comprises the 25 following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

30 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

35 said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid

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which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 32, SEQ ID NO: 33, a sequence complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or 5 representatives of *Streptococcus pyogenes*, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label 10 being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and
c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of 15 the presence and/or amount of *Streptococcus pyogenes* in said test sample.

58. A method as defined in claim 57, wherein said probe is selected from the group consisting of:

20 1) an oligonucleotide of 12-1337 nucleotides in length which sequence is comprised in SEQ ID NO: 32 or a complementary sequence thereof,
25 2) an oligonucleotide of 12-1837 nucleotides in length which sequence is comprised in SEQ ID NO: 33 or a complementary sequence thereof, and variants thereof which specifically and ubiquitously anneal with strains and representatives of *Streptococcus pyogenes*.

30 59. A method for detecting the presence and/or amount of *Streptococcus pyogenes* in a test sample which comprises the following steps:

35 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Streptococcus pyogenes* DNA that

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contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers 5 being chosen from within one of the following sequences: SEQ ID NO: 32 and SEQ ID NO: 33;

10 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

15 c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Streptococcus pyogenes* in said test sample.

15 60. The method of claim 59, wherein said at least one pair of primers is selected from the group consisting of:

- a) SEQ ID NO: 141 and SEQ ID NO: 142, and
- b) SEQ ID NO: 143 and SEQ ID NO: 144.

20 61. A method for the detection, identification and/or quantification of *Enterococcus faecalis* directly from a test sample or from bacterial colonies, which comprises the following steps:

25 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

30 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

35 said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, a sequence

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complementary thereof, a part thereof and a variant thereof, which specifically and ubiquitously anneals with strains or representatives of *Enterococcus faecalis*, under conditions such that the nucleic acid of said probe can selectively 5 hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second 10 reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of *Enterococcus faecalis* in said test sample.

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62. A method as defined in claim 61, wherein said probe is selected from the group consisting of:

1) an oligonucleotide of 12-1817 nucleotides in length which sequence is comprised in SEQ ID NO: 1 or a complementary 20 sequence thereof,

2) an oligonucleotide of 12-2275 nucleotides in length which sequence is comprised in SEQ ID NO: 2, and

variants thereof which specifically and ubiquitously anneal with strains and representatives of *Enterococcus faecalis*. 25

63. A method for detecting the presence and/or amount of *Enterococcus faecalis* in a test sample which comprises the following steps:

30 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of *Enterococcus faecalis* DNA that 35 contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target

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sequence as a template, said at least one pair of primers being chosen from within one of the following sequences: SEQ ID NO: 1 and SEQ ID NO: 2;

5 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

10 c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of *Enterococcus faecalis* in said test sample.

64. The method of claim 63, wherein said at least one pair of primers is selected from the group consisting of:

15 a) SEQ ID NO: 38 and SEQ ID NO: 39, and
b) SEQ ID NO: 40 and SEQ ID NO: 41.

65. A method for the detection of the presence and/or amount of any bacterial species directly from a test sample or from bacterial colonies, which comprises the following steps:

20 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or
inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,
said bacterial DNA being in a substantially single stranded form;

25 b) contacting said single stranded DNA with a universal probe which sequence is selected from the group consisting of SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130 and a sequence complementary thereof, under conditions such that the 30 nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being

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present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

5 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of the presence and/or amount of said any bacterial species in said test sample.

10 66. A method for detecting the presence and/or amount of any bacterial species in a test sample which comprises the following steps:

15 a) treating said sample with an aqueous solution containing a pair of universal primers which sequence is defined in SEQ ID NO: 126 and SEQ ID NO: 127, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said any bacterial species DNA that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template;

20 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

25 c) detecting the presence and/or amount of said amplified target sequence as an indication of the presence and/or amount of said any bacterial species in said test sample.

30 67. A method for evaluating a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *blatem* (TEM-1) directly from a test sample or from bacterial colonies, which comprises the following steps:

35 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

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inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

5 said bacterial DNA being in a substantially single stranded form;

 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group 10 consisting of SEQ ID NO: 161, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a β -lactamase, under conditions such that the nucleic acid of said probe can selectively hybridize with said 15 bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said 20 probe; and

 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene TEM-1.

25 68. A method as defined in claim 67, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 161.

30 69. A method for evaluating a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *blatem* (TEM-1) in a test sample which comprises the following steps:

 a) treating said sample with an aqueous solution 35 containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two

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complementary strands of said bacterial antibiotic resistance gene coding for a β -lactamase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 161;

5 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, 10 and amplifying said target sequence, if any, to a detectable level; and

15 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene TEM-1.

70. A method for evaluating a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *blarob* (ROB-1) directly from a test sample or from 20 bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

25 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

30 said bacterial DNA being in a substantially single stranded form;

35 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 162, a sequence complementary thereto, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a β -lactamase, under conditions such that the

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nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

10 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene ROB-1.

15 71. A method as defined in claim 70, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 162.

20 72. A method for evaluating a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *blarob* (ROB-1) in a test sample which comprises the following steps:

25 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a β -lactamase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said 30 at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 162;

35 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to

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β -lactam antibiotics mediated by the bacterial antibiotic resistance gene ROB-1.

73. A method for evaluating a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *blas_{hv}* (SHV-1) directly from a test sample or from bacterial colonies, which comprises the following steps:

5 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a 10 substantially homogenous population of bacteria isolated from this sample, or

10 15 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

 said bacterial DNA being in a substantially single stranded form;

20 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 163, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a β -lactamase, under conditions such that the 25 nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive 30 member reacting with a second reactive member present on said probe; and

35 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene SHV-1.

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74. A method as defined in claim 73, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 163.

5 75. A method for evaluating a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *blashv* (SHV-1) in a test sample which comprises the following steps:

10 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a β -lactamase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 163;

20 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

25 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene SHV-1.

30 76. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aadB* directly from a test sample or from bacterial colonies, which comprises the following steps:

35 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

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inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

5 said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group 10 consisting of SEQ ID NO: 164, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside adenylyltransferase, under conditions such that the nucleic acid of said probe can 15 selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a 20 second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aadB*.

25 77. A method as defined in claim 76, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 164.

30 78. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aadB* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution 35 containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two

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complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside adenylyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so 5 as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 164;

10 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

15 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aadB*.

79. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial 20 antibiotic resistance gene *aacC1* directly from a test sample or from bacterial colonies, which comprises the following steps:

25 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

30 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

35 said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 165, a sequence complementary 35 thereof, a part thereof and a variant thereof, which

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specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a 5 hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

10 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC1.

15 80. A method as defined in claim 79, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 165.

20 81. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC1—in a test sample which comprises the following steps:

25 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase that contains a target sequence, and the other of said primers 30 being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 165;

35 b) synthesizing an extension product of each of said primers which extension products contain the target sequence,

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and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to 5 aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC1.

82. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial 10 antibiotic resistance gene aacC2 directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a 15 substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated 20 bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid 25 which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 166, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase, under 30 conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said 35 labelling means, said first reactive member reacting with a second reactive member present on said probe; and

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c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC2.

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83. A method as defined in claim 82, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 166.

10 84. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC2 in a test sample which comprises the following steps:

15 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase that 20 contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 25 166;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

30 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC2.

35 85. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC3 directly from a test sample

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or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a 5 substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated 10 bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid 15 which nucleotidic sequence is selected from the group consisting of SEQ. ID NO: 167, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase, under 20 conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said 25 labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label 30 on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacC3.

86. A method as defined in claim 85, wherin said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 167.

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87. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial

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antibiotic resistance gene *aacC3* in a test sample which comprises the following steps:

- a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having 5 at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase that contains a target sequence, and the other of said primers 10 being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 167;
- b) synthesizing an extension product of each of said 15 primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and
- c) detecting the presence and/or amount of said amplified 20 target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacC3* .

88. A method for evaluating a bacterial resistance to 25 aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacA4* directly from a test sample or from bacterial colonies, which comprises the following steps:

- a) depositing and fixing on an inert support or leaving 30 in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or
- inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated 35 bacteria to release the bacterial DNA,

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said bacterial DNA being in a substantially single stranded form;

5 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 168, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase, under 10 conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said 15 labelling means, said first reactive member reacting with a second reactive member present on said probe; and

20 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacA4 .

89. A method as defined in claim 88, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 168.

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90. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacA4 in a test sample which comprises the following steps:

30 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so

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as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 168;

5 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

10 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene aacA4.

91. A method for evaluating a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *mecA* directly from a test sample or from bacterial colonies, which comprises the following steps:

15 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

20 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

25 said bacterial DNA being in a substantially single stranded form;

30 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 169, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a penicillin-binding protein, under conditions 35 such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling

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means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

5 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *mecA*.

10 92. A method as defined in claim 91, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 169.

15 93. A method for evaluating a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *mecA* in a test sample which comprises the following steps:

20 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a penicillin-binding protein that contains a target sequence, and the other of said primers being capable 25 of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 169;

30 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

35 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to β -lactam antibiotics mediated by the bacterial antibiotic resistance gene *mecA*.

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94. A method for evaluating a bacterial resistance to vancomycin mediated by the bacterial antibiotic resistance genes vanH, vanA and vanX directly from a test sample or from bacterial colonies, which comprises the following steps:

5 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

10 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

15 said bacterial DNA being in a substantially single stranded form;

15 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 170, a sequence complementary thereof, a part thereof and a variant thereof, which 20 specifically anneals with said bacterial antibiotic resistance genes coding for vancomycin-resistance proteins, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected 25 by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

30 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to vancomycin mediated by the bacterial antibiotic resistance genes vanH, vanA and vanX.

95. A method as defined in claim 94, wherein said probe 35 comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 170.

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96. A method for evaluating a bacterial resistance to vancomycin mediated by the bacterial antibiotic resistance genes vanH, vanA and vanX in a test sample which comprises the following steps:

- 5 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance genes coding for vancomycin-resistance proteins that contain a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 170;
- 10 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and
- 15 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to vancomycin mediated by the bacterial antibiotic resistance genes vanH, vanA and vanX.

25 97. A method for evaluating a bacterial resistance to streptogramin A mediated by the bacterial antibiotic resistance gene satA directly from a test sample or from bacterial colonies, which comprises the following steps:

- 30 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or
- 35 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing in situ said inoculated sample or isolated bacteria to release the bacterial DNA,

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said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 173, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a streptogramin A acetyltransferase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to streptogramin A mediated by the bacterial antibiotic resistance gene *satA*.

98. A method as defined in claim 97, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 173.

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99. A method for evaluating a bacterial resistance to streptogramin A mediated by the bacterial antibiotic resistance gene *satA* in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for streptogramin A acetyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so

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as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 173;

5 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

10 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to streptogramin A mediated by the bacterial antibiotic resistance gene *satA*.

100. A method for evaluating a bacterial resistance to 15. aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacA-aphD* directly from a test sample or from bacterial colonies, which comprises the following steps:

20 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

25 b) inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

 said bacterial DNA being in a substantially single stranded form;

30 c) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 174, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an aminoglycoside acetyltransferase-phosphotransferase under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial

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DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

5 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to aminoglycoside antibiotics mediated 10 by the bacterial antibiotic resistance gene *aacA-aphD*.

101. A method as defined in claim 100, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 174.

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102. A method for evaluating a bacterial resistance to aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacA-aphD* in a test sample which comprises the following steps:

20 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance 25 gene coding for an aminoglycoside acetyltransferase-phosphotransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one 30 pair of primers being chosen from within the sequence defined in SEQ ID NO: 174;

35 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to

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aminoglycoside antibiotics mediated by the bacterial antibiotic resistance gene *aacA-aphD*.

103. A method for evaluating a bacterial resistance to 5 virginiamycin mediated by the bacterial antibiotic resistance gene *vat* directly from a test sample or from bacterial colonies, which comprises the following steps:

a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a 10 substantially homogenous population of bacteria isolated from this sample, or

inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated 15 bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid 20 which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 175, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for a virginiamycin acetyltransferase, under 25 conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said 30 labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to virginiamycin mediated by the 35 bacterial antibiotic resistance gene *vat*.

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104. A method as defined in claim 103, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 175.

5 105. A method for evaluating a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene vat in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for a virginiamycin acetyltransferase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 175;

20 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

25 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene vat.

30 106. A method for evaluating a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene vga directly from a test sample or from bacterial colonies, which comprises the following steps:

35 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

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inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

5 said bacterial DNA being in a substantially single stranded form;

b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group 10 consisting of SEQ ID NO: 176, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an ATP-binding protein, under conditions such that the nucleic acid of said probe can selectively hybridize 15 with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present 20 on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene vga.

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107. A method as defined in claim 106, therein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 176.

30 108. A method for evaluating a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene vga in a test sample which comprises the following steps:

a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having 35 at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance

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gene coding for an ATP-binding protein that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 176;

5 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

10 c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to virginiamycin mediated by the bacterial antibiotic resistance gene vga.

15 109. A method for evaluating a bacterial resistance to erythromycin mediated by the bacterial antibiotic resistance gene msra directly from a test sample or from bacterial colonies, which comprises the following steps:

20 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

25 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

30 said bacterial DNA being in a substantially single stranded form;

35 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 177, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance gene coding for an erythromycin resistance protein under conditions such that the nucleic acid of said probe can

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selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first reactive member of said 5 labelling means, said first reactive member reacting with a second reactive member present on said probe; and

c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of a bacterial resistance to erythromycin mediated by the 10 bacterial antibiotic resistance gene *msrA*.

110. A method as defined in claim 109, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 177.

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111. A method for evaluating a bacterial resistance to erythromycin mediated by the bacterial antibiotic resistance gene *msrA* in a test sample which comprises the following steps:

20 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance

25 gene coding for an erythromycin resistance protein that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers

30 being chosen from within the sequence defined in SEQ ID NO: 177;

35 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of a bacterial resistance to

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erythromycin mediated by the bacterial antibiotic resistance gene *msrA*.

112. A method for evaluating potential bacterial resistance to
5 β -lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *int* directly from a test sample or from bacterial colonies, which comprises the following steps:

10 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a substantially homogenous population of bacteria isolated from this sample, or

15 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

20 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 171, a sequence complementary thereof, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance 25 gene coding for an integrase, under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or the label being present on a first 30 reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

35 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of potential bacterial resistance to β -lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *int*.

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113. A method as defined in claim 112, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 171.

5 114. A method for evaluating potential bacterial resistance to β -lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *int* in a test sample which comprises the following steps:

10 a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two complementary strands of said bacterial antibiotic resistance gene coding for an integrase that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 171;

15 20 b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable level; and

25 c) detecting the presence and/or amount of said amplified target sequence as an indication of potential bacterial resistance to β -lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *int*.

30 30 115. A method for evaluating potential bacterial resistance to β -lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *sul* directly from a test sample or from bacterial colonies, which comprises the following steps:

35 a) depositing and fixing on an inert support or leaving in solution the bacterial DNA of the sample or of a

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substantially homogenous population of bacteria isolated from this sample, or

5 inoculating said sample or said substantially homogenous population of bacteria isolated from this sample on an inert support, and lysing *in situ* said inoculated sample or isolated bacteria to release the bacterial DNA,

said bacterial DNA being in a substantially single stranded form;

10 b) contacting said single stranded DNA with a probe, said probe comprising at least one single stranded nucleic acid which nucleotidic sequence is selected from the group consisting of SEQ ID NO: 172, a sequence complementary thereto, a part thereof and a variant thereof, which specifically anneals with said bacterial antibiotic resistance 15 gene coding for a sulfonamide resistance protein under conditions such that the nucleic acid of said probe can selectively hybridize with said bacterial DNA, whereby a hybridization complex is formed, said complex being detected by labelling means, the label being present on said probe or 20 the label being present on a first reactive member of said labelling means, said first reactive member reacting with a second reactive member present on said probe; and

25 c) detecting the presence or the intensity of said label on said inert support or in said solution as an indication of potential bacterial resistance to β -lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *sul*.

30 116. A method as defined in claim 115, wherein said probe comprises an oligonucleotide of at least 12 nucleotides in length which hybridizes to SEQ ID NO: 172.

35 117. A method for evaluating potential bacterial resistance to β -lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic resistance gene *sul* in a test sample which comprises the following steps:

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a) treating said sample with an aqueous solution containing at least one pair of oligonucleotide primers having at least 12 nucleotides in length, one of said primers being capable of hybridizing selectively with one of the two 5 complementary strands of said bacterial antibiotic resistance gene coding for a sulfonamide resistance protein that contains a target sequence, and the other of said primers being capable of hybridizing with the other of said strands so as to form an extension product which contains the target sequence as a 10 template, said at least one pair of primers being chosen from within the sequence defined in SEQ ID NO: 172;

b) synthesizing an extension product of each of said primers which extension products contain the target sequence, and amplifying said target sequence, if any, to a detectable 15 level; and

c) detecting the presence and/or amount of said amplified target sequence as an indication of potential bacterial resistance to β -lactams, aminoglycosides, chloramphenicol and/or trimethoprim mediated by the bacterial antibiotic 20 resistance gene sul.

118. A nucleic acid having the nucleotide sequence of any one of SEQ ID NOS: 1 to 37, SEQ ID NOS: 161 to 177, a part thereof and variants thereof which, when in single stranded form, 25 ubiquitously and specifically hybridize with a target bacterial DNA as a probe or as a primer.

119. An oligonucleotide having a nucleotidic sequence of any one of SEQ ID NOS: 38 to 160.

30 120. A recombinant plasmid comprising a nucleic acid as defined in claim 118.

121. A recombinant host which has been transformed by a 35 recombinant plasmid according to claim 120.

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122. A recombinant host according to claim 121 wherein said host is *Escherichia coli*.

123. A diagnostic kit for the detection and/or quantification 5 of the nucleic acids of any combination of the bacterial species defined in any one of claims 9, 14, 19, 24, 29, 34, 39, 43, 47, 52, 57 and 61, comprising any combination of probes defined therein.

10 124. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial species defined in any one of claims 10, 11, 15, 16, 20, 21, 25, 26, 30, 31, 35, 36, 40, 44, 48, 49, 53, 54, 58, 62 and 65, comprising any combination of oligonucleotide probes defined 15 therein.

125. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial species defined in any one of claims 12, 13, 17, 18, 22, 23, 20 27, 28, 32, 33, 37, 38, 41, 42, 45, 46, 50, 51, 55, 56, 59, 60, 63, 64 and 66 comprising any combination of primers defined therein.

126. A diagnostic kit for the detection and/or quantification 25 of the nucleic acids of any combination of the bacterial resistance genes defined in any one of claims 67, 70, 73, 76, 79, 82, 85, 88, 91, 94, 97, 100, 103, 106 and 109 comprising 79 any combination of probes defined therein.

30 127. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial resistance genes defined in any one of claims 68, 71, 74, 77, 80, 83, 86, 89, 92, 95, 98, 101, 104, 107 and 110 comprising 83 any combination of oligonucleotide probes defined therein.

35 128. A diagnostic kit for the detection and/or quantification of the nucleic acids of any combination of the bacterial

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resistance genes defined in any one of claims 69, 72, 75, 78, 81, 84, 87, 90, 93, 96, 99, 102, 105, 108 and 111 comprising any combination of primers defined therein.

5 129. A diagnostic kit for the simultaneous detection and quantification of nucleic acids of any combination of the bacterial species defined in claim 123, comprising any combination of the bacterial probes defined therein and any combination of the probes to the antibiotic resistance genes
10 defined in any one of SEQ ID NOS: 161 to 177 in whole or in part.

15 130. A diagnostic kit for the simultaneous detection and quantification of nucleic acids of any combination of the bacterial species defined in claim 124, comprising any combination of the bacterial oligonucleotide probes defined therein and any combination of oligonucleotide probes that hybridize to the antibiotic resistance genes defined in any one of SEQ ID NOS: 161 to 177.

20 131. A diagnostic kit for the simultaneous detection and quantification of nucleic acids of any combination of the bacterial species defined in claim 125, comprising any combination of the primers defined therein and any combination of primers that anneal to the antibiotic resistance genes
25 defined in any one of SEQ ID NOS: 161 to 177.

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